GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 28, 2004, 21:07:45 ; Search time 54 Seconds
(without alignments)
1258.055 Million cell updates/sec

Title: US-10-056-884A-2
Perfect score: 2284
Sequence: 1 MALSGNCSRYYPREQGSAVP.....DRFPERKHPWQSELLRKYHL 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2284	100.0	428	23	AAE28618	Human K+betaM2 pro
2	2271	99.4	428	23	ABB97351	Novel human protei
3	2271	99.4	435	23	ABJ10888	K+beta M6 related
4	1285	56.3	473	24	AAE32081	Human TRICH-15 pro
5	1242	54.4	301	22	ABB11972	Human VM106R.1 hom
6	832	36.4	325	23	ABJ10886	K+beta M6 protein
7	541	23.7	103	23	AAE28628	Human K+betaM2 pro
8	538.5	23.6	228	22	ABB60184	Drosophila melanog
9	538.5	23.6	228	23	ABJ10887	K+beta M6 related
10	367	16.1	101	23	ABJ10893	K+beta M6 related
11	232	10.2	272	22	AAM25877	Human protein sequ
12	231	10.1	290	23	ABP69573	Human polypeptide
13	231	10.1	339	22	AAE10329	Human transporter
14	210.5	9.2	283	21	AAB41802	Human ORFX ORF1566
15	210	9.2	256	20	AAY34125	Human potassium ch
16	210	9.2	256	23	ABJ10890	K+beta M6 related
17	210	9.2	257	21	AAY70452	Human membrane cha
18	210	9.2	257	22	AAM40284	Human polypeptide
19	210	9.2	257	23	ABP53971	Human membrane cha
20	210	9.2	257	24	AAG79900	Human MECHP2. Hom
21	210	9.2	287	24	ABR41784	Human DITHP growth
22	210	9.2	302	22	ABG02913	Novel human diagno
23	210	9.2	404	22	AAM42070	Human polypeptide
24	204	8.9	213	22	AAE04898	Human transporter
25	204	8.9	213	23	ABG70920	Human novel membra
26	204	8.9	213	23	ABB78788	Human macroprotein
27	203	8.9	252	23	ABP51311	Human MDDT SEQ ID
28	203	8.9	528	24	AAG79897	Ion channel 47619.
29	202.5	8.9	237	20	AAY34129	Human potassium ch
30	202.5	8.9	237	22	AAU27754	Human full-length
31	202.5	8.9	237	22	AAM93682	Human polypeptide,
32	202.5	8.9	237	22	AAB95201	Human protein sequ
33	202.5	8.9	237	23	ABP53973	Human beta subunit
34	202.5	8.9	237	23	ABJ10891	K+beta M6 related
35	202.5	8.9	237	23	ABJ10892	K+beta M6 related
36	202.5	8.9	237	23	ABP51811	Human potassium ch
37	201.5	8.8	257	23	ABG70925	Human novel membra
38	201.5	8.8	283	22	AAB95629	Human protein sequ
39	201.5	8.8	283	23	ABG70923	Human novel membra
40	201.5	8.8	283	23	ABG61546	Human transporter
41	193.5	8.5	140	23	ABJ10889	K+beta M6 related
42	193.5	8.5	237	22	AAM93832	Human polypeptide,
43	191	8.4	75	23	ABP34708	Human ORF3681 prot
44	189	8.3	190	22	ABG16368	Novel human diagno
45	189	8.3	205	22	AAM41795	Human polypeptide

ALIGNMENTS

RESULT 1
AAE28618
ID AAE28618 standard; Protein; 428 AA.
XX
AC AAE28618;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human K+betaM2 protein.
XX
KW Human; potassium channel beta-subunit; K+betaM2 protein; neural disorder;
KW reproductive disorder; metabolic disorder; premature puberty; nephritis;
KW endocrine disorder; memory disorder; neuroendocrine condition; asthma;
KW spermatogenesis; renal disease; learning deficiency; Alzheimer's disease;
KW neurodegenerative disease; proliferative disorder; autoimmune disease;
KW carcinoid tumour; blood coagulation disease; blood platelet disease;
KW rheumatoid arthritis; allergy; hyperproliferative disease; gene therapy;
KW graft-versus-host disease; organ rejection; antisterility; thrombolytic;
KW antiinflammatory; neuroprotective; anti-Parkinsonian; immunosuppressive;
KW nephrotropic; cytostatic; nootropic; hypotensive; vulnerary.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Domain   25..127
FT   /label= Potassium_channel_tetramerisation_domain
FT Domain   243..263
FT   /label= Transmembrane_domain
XX
PN WO200266601-A2.
XX
PD 29-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US02332.
XX
PR 24-JAN-2001; 2001US-263872P.
PR 14-FEB-2001; 2001US-269794P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Feder J, Lee L, Chen J, Jackson D, Ramanathan C, Siemers N;
PI Chang H, Carroll P;
XX
DR WPI; 2002-691617/74.
DR N-PSDB; AAD46068.
XX
PT New potassium channel beta-subunit, K+betaM2, proteins and nucleic
PT acids, useful for diagnosing, treating and/or preventing e.g.
PT reproductive, neural, metabolic, endocrine, memory, neurodegenerative
PT disorders or diseases -
XX
PS Claim 5; Page 347-349; 366pp; English.
XX
CC The present invention relates to human potassium channel beta-subunit
CC (K+betaM2) proteins and polynucleotides encoding such proteins. The
CC K+betaM2 sequences are useful for diagnosing, treating and/or preventing
CC reproductive disorders, neural disorders, disorders related to aberrant

CC potassium regulation or hyper potassium channel activity, metabolic
CC disorders (e.g. premature puberty), endocrine disorders (e.g. aberrant
CC growth hormone synthesis and/or secretion), memory disorder, disorders
CC of the testis (e.g. spermatogenesis), neuroendocrine condition related
CC to aberrant thyroid hormone release, renal disease or disorders (e.g.
CC nephritis), disorders related to aberrant higher brain function (e.g.
CC learning deficiencies), neurodegenerative diseases (e.g. Alzheimer's
CC disease), proliferative disorders (e.g. carcinoid tumour) and disorders
CC involving excessive smooth muscle tone or excitability (e.g. asthma).
CC They may be used to modulate haemostatic or thrombolytic activity, to
CC treat or prevent blood coagulation diseases or disorders, blood platelet
CC diseases, wounds, autoimmune diseases, disorders or conditions (e.g.
CC rheumatoid arthritis), allergic reactions (e.g. asthma), organ rejection
CC or graft-versus-host disease, and hyperproliferative diseases. K+betaM2
CC sequences are also used in gene therapy. The present sequence is human
CC K+betaM2 protein.
XX
SQ Sequence 428 AA;

Query Match 100.0%; Score 2284; DB 23; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.9e-220;
Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 60

Qy         61 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVK 120

Qy        121 LLTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREG 180

Qy        181 QADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFKHLERAFDML 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFKHLERAFDML 240

Qy        241 SECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 300

Qy        301 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEMR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEMR 360

Qy        361 RKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 RKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS 420

Qy        421 ELLRKYHL 428
              ||||||||
Db        421 ELLRKYHL 428
```

RESULT 2

```
ABB97351
ID   ABB97351 standard; Protein; 428 AA.
XX
AC   ABB97351;
XX
DT   27-JUN-2002  (first entry)
XX
DE   Novel human protein SEQ ID NO: 619.
XX
KW   Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
KW   antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KW   neuroprotective; antiparkinsonian; protein therapy; EST;
KW   expressed sequence tag.
XX
OS   Homo sapiens.
XX
PN   WO200222660-A2.
XX
PD   21-MAR-2002.
XX
PF   10-SEP-2001; 2001WO-US26015.
XX
PR   11-SEP-2000; 2000US-0659671.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Zhou P,  Asundi V,  Zhang J,  Zhao QA,  Ren F;
PI   Xue AJ,  Yang Y,  Wehrman T,  Drmanac RT;
XX
DR   WPI; 2002-292408/33.
DR   N-PSDB; ABN32537.
XX
PT   An isolated polynucleotide for treating diseases associated with its
PT   encoded polypeptide such as cancer and multiple sclerosis -
XX
PS   Example 2; SEQ ID NO 619; 509pp; English.
XX
CC   The present invention provides the protein and coding sequences of 444
CC   novel human proteins. These were isolated from expressed sequences tags
CC   (ESTs). They can be used to stimulate cell growth, to regulate
CC   haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
CC   e.g. in burn treatment, to regulate the immune system e.g. to treat
CC   multiple sclerosis, to regulate activin or inhibin e.g. to treat
CC   infertility, to regulate haemostasis or thrombolysis e.g. to treat
CC   stroke and cancer, to screen for drugs, to treat inflammatory conditions
CC   e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
CC   Parkinson's disease. The present sequence is a protein of the invention.
XX
SQ   Sequence   428 AA;

  Query Match             99.4%;  Score 2271;  DB 23;  Length 428;
  Best Local Similarity   99.5%;  Pred. No. 3.8e-219;
  Matches  426;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 60
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Db          1 MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 60
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Qy         61 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVK 120
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Db         61 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVK 120

Qy        121 LLTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREG 180

Qy        181 QADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFKHLERAFDML 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFKHLERAFDML 240

Qy        241 SECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 300
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Db        241 SECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 300

Qy        301 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEMR 360
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Db        301 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEMR 360

Qy        361 RKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS 420
              ||||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        361 RKSDLLRTLTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKIKIPDRFPERKHPWQS 420

Qy        421 ELLRKYHL 428
              ||||||||
Db        421 ELLRKYHL 428
```

RESULT 3
ABJ10888
ID ABJ10888 standard; Protein; 435 AA.
XX
AC ABJ10888;
XX
DT 05-DEC-2002 (first entry)
XX
DE K+beta M6 related protein SEQ ID No 4.
XX
KW Cytostatic; cardiant; neuroprotective; immunomodulator; antimigraine;
KW sedative; gynaecological;; potassium channel beta subunit; K+betaM6;
KW gastrointestinal; reproductive; neural; sleep; low DNA repair capacity;
KW hyperpotassium channel activity; cardiovascular; melatonin synthesis;
KW mammary cancer tumourigenesis; pineal gland associated disorder;
KW pulmonary disorder; immune disorder; NF-kB activity; migraine headache;
KW low free-radical buffering capacity; delayed sleep phase syndrome;
KW circadian cycle; melatonin secretion; cancer.
XX
OS Homo sapiens.
XX
PN WO200270727-A2.
XX
PD 12-SEP-2002.
XX
PF 21-FEB-2002; 2002WO-US05674.
XX

PR 21-FEB-2001; 2001US-270132P.
PR 27-MAR-2001; 2001US-278953P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Feder J, Lee L, Chen J, Jackson DG, Ramanathan C, Siemers N;
PI Chang H;
XX
DR WPI; 2002-713455/77.
XX
PT New polynucleotide encoding human potassium channel beta subunit
PT polypeptide, useful for diagnosing, preventing, treating or
PT ameliorating e.g. cancer -
XX
PS Disclosure; Fig 2; 332pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding a potassium
CC channel beta subunit (K+betaM6) polypeptide or its variants. The human
CC potassium beta subunit polynucleotide or polypeptide is useful for
CC diagnosing, preventing, treating or ameliorating a pathological condition
CC such as gastrointestinal, reproductive, neural, sleep, cardiovascular or
CC pulmonary disorders, a disorder related to hyperpotassium channel
CC activity, an immune disorder related to aberrant NF-kB activity, pineal
CC gland associated disorders, migraine headaches, disorders associated with
CC aberrant melatonin synthesis and/or release or with low DNA repair
CC capacities or low free-radical buffering capacity, delayed sleep phase
CC syndrome, aberrations in circadian cycle, mammary cancer tumourigenesis,
CC age related disorders associated with decreased melatonin secretion, or
CC cancer. This sequence represents a potassium channel beta subunit
CC (K+betaM6) related protein of the invention.
XX
SQ Sequence 435 AA;

Query Match 99.4%; Score 2271; DB 23; Length 435;
Best Local Similarity 99.5%; Pred. No. 3.9e-219;
Matches 426; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 60
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Db          8 MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 67

Qy         61 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVK 120
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Db         68 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVK 127

Qy        121 LLTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 LLTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREG 187

Qy        181 QADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFKHLERAFDML 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 QADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFKHLERAFDML 247

Qy        241 SECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 SECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 307
```

```
Qy        301 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEMR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEMR 367

Qy        361 RKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS 420
              ||||||| ||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        368 RKSDLLRTLTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKIKIPDRFPERKHPWQS 427

Qy        421 ELLRKYHL 428
              ||||||||
Db        428 ELLRKYHL 435


RESULT 4
AAE32081
ID   AAE32081 standard; Protein; 473 AA.
XX
AC   AAE32081;
XX
DT   24-MAR-2003  (first entry)
XX
DE   Human TRICH-15 protein.
XX
KW   Human; transporter and ion channel; TRICH; atherosclerosis; cancer;
KW   gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..39
FT                   /label= Signal_peptide
FT   Protein         40..473
FT                   /note= "Mature human TRICH protein"
FT   Domain          44..151
FT                   /note= "K+ channel tetramerisation domain"
XX
PN   WO200283712-A2.
XX
PD   24-OCT-2002.
XX
PF   12-APR-2002; 2002WO-US11760.
XX
PR   12-APR-2001; 2001US-283440P.
PR   20-APR-2001; 2001US-285592P.
PR   27-APR-2001; 2001US-287263P.
PR   04-MAY-2001; 2001US-288666P.
PR   18-MAY-2001; 2001US-292042P.
PR   25-MAY-2001; 2001US-293724P.
PR   22-JAN-2002; 2002US-351107P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Baughn MR, Elliott VS, Hafalia AJA, Yang J, Walia NK, Ramkumar J;
PI   Forsythe IJ, Lu Y, Tang YT, Yue H, Raumann BE, Lal PG, Azimzai Y;
PI   Lu DAM, Gandhi AR, Thornton M, Nguyen DB, Arvizu CS, Emerling BM;
PI   Swarnakar A, Yao MG, Ding L, He A, Griffin JA, Sanjanwala MM;
PI   Gietzen KJ, Lee EA, Xu Y, Au-Young JK, Das D, Lee SY, Chang H;
```

XX
DR WPI; 2003-092996/08.
DR N-PSDB; AAD49513.
XX
PT New human functional transporters and ion channels (TRICH)
PT polypeptides, useful for preparing a composition for diagnosing or
PT treating a disease associated with decreased expression or
PT overexpression of TRICH e.g. cancer -
XX
PS Claim 1; Page 177-178; 204pp; English.
XX
CC The invention relates to human transporters and ion channels (TRICH)
CC polypeptides and nucleic acid molecules encoding such polypeptides.
CC TRICH proteins are useful for preparing compositions for diagnosing or
CC treating diseases or conditions associated with decreased expression
CC or overexpression of functional TRICH e.g. atherosclerosis or cancer.
CC The invention is useful in gene therapy. The present sequence is
CC human TRICH protein.
XX
SQ Sequence 473 AA;

Query Match 56.3%; Score 1285; DB 24; Length 473;
Best Local Similarity 60.8%; Pred. No. 6e-120;
Matches 268; Conservative 47; Mismatches 96; Indels 30; Gaps 9;

```
Qy         16 GSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTA-----NDLAKDSK 70
              |   |: |||||||||||||| |:||||:|:| | |  ||||           :| :||:
Db         35 GPCAPSPFPEVVELNVGGQVYVTKHSTLLSVPDSTLASMFSPSSPRGGARRRGELPRDSR 94

Qy         71 GRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQS 130
               ||||||||||||:||||||:|: ||:|||||  || ||||||||  ||||||:|   ||:
Db         95 ARFFIDRDGFLFRYVLDYLRDKQLALPEHFPEKERLLREAEYFQLTDLVKLLSPKVTKQN 154

Qy        131 P--DEFCHSDFED-ASQGSDTRIC--PPSSLLPA--------------DRKWGFITVGYR 171
                 || | || ||  ||||   :     :: :|:               |:: ||:|:|||
Db        155 SLNDEGCQSDLEDNVSQGSSDALLLRGAAAAVPSGPGAHGGGGGGGAQDKRSGFLTLGYR 214

Qy        172 GSCTLGREGQADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFK 231
               || |  |: ||||||||| ||:|||||:|||||||:|||||||||| ||:|||||||||
Db        215 GSYTTVRDNQADAKFRRVARIMVCGRIALAKEVFGDTLNESRDPDRQPEKYTSRFYLKFT 274

Qy        232 HLERAFDMLSECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSR-WSPSHCDC 290
               :||:||| ||| ||||||||||  ||:|:||| ||||||||||:|:| | :  ||
Db        275 YLEQAFDRLSEAGFHMVACNSSGTAAFVNQYRDDKIWSSYTEYIFFRPPQKIVSPKQEHE 334

Qy        291 CCKNGK-GDKEGESGTSCNDLSTSSCDSQSEASSPQETVICG--PVTRQTNIQTLDRPIK 347
                 |: |  ||  |||||||:|||||||| ||||:||:           | |  ||||| |
Db        335 DRKHDKVTDKGSESGTSCNELSTSSCDSHSEASTPQDNPSSAQQATAHQPNTLTLDRPSK 394

Qy        348 KGPVQLIQQSEMRRKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKI 407
               | ||| |   : || |:| : | | |||:|:| ||  | ||||:|||::|||||| |  |
Db        395 KAPVQWIPPPDKRRNSELFQTLISKSRETNLSKKK--VCEKLSVEEEMKKCIQDFKKIHI 452

Qy        408 PDRFPERKHPWQSELLRKYHL 428
               || |||||  ||||||:|| |
Db        453 PDYFPERKRQWQSELLQKYGL 473
```

RESULT 5
ABB11972
ID   ABB11972 standard; peptide; 301 AA.
XX
AC   ABB11972;
XX
DT   11-JAN-2002 (first entry)
XX
DE   Human VM106R.1 homologue, SEQ ID NO:2342.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW   haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW   inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW   proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW   myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW   chronic inflammatory condition; proliferative retinopathy;
KW   atherosclerosis; coronary heart disease; arterial ischaemia;
KW   bone disorder; osteoporosis; vascular growth disorder;
KW   tissue regeneration; wound healing; infection; immune disorder;
KW   cell culture; drug screening; gene therapy; antiinflammatory;
KW   antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW   cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW   antifungal; vulnerary; antiulcer.
XX
OS   Homo sapiens.
XX
PN   WO200157188-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US03800.
XX
PR   03-FEB-2000; 2000US-0496914.
PR   27-APR-2000; 2000US-0560875.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Drmanac RT;
XX
DR   WPI; 2001-457740/49.
DR   N-PSDB; ABA09216.
XX
PT   Human proteins and DNA encoding sequences useful for preventing,
PT   treating or ameliorating a medical condition in a mammalian subject
PT   e.g. arthritis and cancer -
XX
PS   Claim 20; Page 289; 1963pp; English.
XX
CC   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC   sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC   invention also relates to vectors and recombinant host cells comprising a
CC   nucleotide of the invention, methods of producing the novel polypeptides,
CC   antibodies against the polypeptides, methods of detecting the nucleotides
CC   or polypeptides in a sample, and methods of identifying compounds which
CC   bind to polypeptides of the invention. Although novel, many of the
CC   polypeptides of the invention have homology to known proteins, thereby

CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention.
XX
SQ Sequence 301 AA;

Query Match 54.4%; Score 1242; DB 22; Length 301;
Best Local Similarity 100.0%; Pred. No. 6.3e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 60

Qy         61 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVK 120

Qy        121 LLTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREG 180

Qy        181 QADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFKHL 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFKHL 233
```

RESULT 6
ABJ10886
ID ABJ10886 standard; Protein; 325 AA.
XX

AC ABJ10886;
XX
DT 05-DEC-2002 (first entry)
XX
DE K+beta M6 protein SEQ ID No 2.
XX
KW Cytostatic; cardiant; neuroprotective; immunomodulator; antimigraine;
KW sedative; gynaecological;; potassium channel beta subunit; K+betaM6;
KW gastrointestinal; reproductive; neural; sleep; low DNA repair capacity;
KW hyperpotassium channel activity; cardiovascular; melatonin synthesis;
KW mammary cancer tumourigenesis; pineal gland associated disorder;
KW pulmonary disorder; immune disorder; NF-kB activity; migraine headache;
KW low free-radical buffering capacity; delayed sleep phase syndrome;
KW circadian cycle; melatonin secretion; cancer.
XX
OS Homo sapiens.
XX
PN WO200270727-A2.
XX
PD 12-SEP-2002.
XX
PF 21-FEB-2002; 2002WO-US05674.
XX
PR 21-FEB-2001; 2001US-270132P.
PR 27-MAR-2001; 2001US-278953P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Feder J, Lee L, Chen J, Jackson DG, Ramanathan C, Siemers N;
PI Chang H;
XX
DR WPI; 2002-713455/77.
DR N-PSDB; ABT09812.
XX
PT New polynucleotide encoding human potassium channel beta subunit
PT polypeptide, useful for diagnosing, preventing, treating or
PT ameliorating e.g. cancer -
XX
PS Claim 5; Fig 1; 332pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding a potassium
CC channel beta subunit (K+betaM6) polypeptide or its variants. The human
CC potassium beta subunit polynucleotide or polypeptide is useful for
CC diagnosing, preventing, treating or ameliorating a pathological condition
CC such as gastrointestinal, reproductive, neural, sleep, cardiovascular or
CC pulmonary disorders, a disorder related to hyperpotassium channel
CC activity, an immune disorder related to aberrant NF-kB activity, pineal
CC gland associated disorders, migraine headaches, disorders associated with
CC aberrant melatonin synthesis and/or release or with low DNA repair
CC capacities or low free-radical buffering capacity, delayed sleep phase
CC syndrome, aberrations in circadian cycle, mammary cancer tumourigenesis,
CC age related disorders associated with decreased melatonin secretion, or
CC cancer. This sequence represents the potassium channel beta subunit
CC (K+betaM6) protein of the invention.
XX
SQ Sequence 325 AA;

```
  Query Match             36.4%;  Score 832;  DB 23;  Length 325;
  Best Local Similarity   54.0%;  Pred. No. 1.2e-74;
  Matches  170;  Conservative   41;  Mismatches   56;  Indels   48;  Gaps    6;

Qy          4 SGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTAN 63
              ||: |        || |  ||::|||||||||| ||  |::|:| ||||:||: ::
Db         20 SGSSS-------SSAEPPLFPDIVELNVGGQVYVTRRCTVVSVPDSLLWRMFTQQQ--PQ 70

Qy         64 DLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLL- 122
              :||:|||||||:|||||||||||||||| |:||||:|||: ||:||||||:||:||: |
Db         71 ELARDSKGRFFLDRDGFLFRYILDYLRDLQLVLPDYFPERSRLEREAEYFELPELVRRLG 130

Qy        123 TPDEIKQSP--------------DEFCHSDFEDASQ----------------------GS 146
               | :    |               ||     : :  |                      |:
Db        131 APQQPGPGPPPSRRGVHKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGA 190

Qy        147 DTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVFG 206
                 :  ||  |   |: |:||:||||| |:||: ||||||||| || |||: ||||||||
Db        191 AGPLLTPSQSLDGSRRSGYITIGYRGSYTIGRDAQADAKFRRVARITVCGKTSLAKEVFG 250

Qy        207 ETLNESRDPDRAPERYTSRFYLKFKHLERAFDMLSECGFHMVACNSSVTASFIN--QYTD 264
              :|||||||||| |||||||:||||  ||:||| ||| |||||||:|: | :| :    ::
Db        251 DTLNESRDPDRPPERYTSRYYLKFNFLEQAFDKLSESGFHMVACSSTGTCAFASSTDQSE 310

Qy        265 DKIWSSYTEYVFYRE 279
              ||||:||||||| ||
Db        311 DKIWTSYTEYVFCRE 325


RESULT 7
AAE28628
ID   AAE28628 standard; Protein; 103 AA.
XX
AC   AAE28628;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human K+betaM2 protein fragment.
XX
KW   Human; potassium channel beta-subunit; K+betaM2 protein; neural disorder;
KW   reproductive disorder; metabolic disorder; premature puberty; nephritis;
KW   endocrine disorder; memory disorder; neuroendocrine condition; asthma;
KW   spermatogenesis; renal disease; learning deficiency; Alzheimer's disease;
KW   neurodegenerative disease; proliferative disorder; autoimmune disease;
KW   carcinoid tumour; blood coagulation disease; blood platelet disease;
KW   rheumatoid arthritis; allergy; hyperproliferative disease; gene therapy;
KW   graft-versus-host disease; organ rejection; antisterility; thrombolytic;
KW   antiinflammatory; neuroprotective; anti-Parkinsonian; immunosuppressive;
KW   nephrotropic; cytostatic; nootropic; hypotensive; vulnerary.
XX
OS   Homo sapiens.
XX
PN   WO200266601-A2.
XX
PD   29-AUG-2002.
XX
PF   24-JAN-2002; 2002WO-US02332.
```

XX
PR 24-JAN-2001; 2001US-263872P.
PR 14-FEB-2001; 2001US-269794P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Feder J, Lee L, Chen J, Jackson D, Ramanathan C, Siemers N;
PI Chang H, Carroll P;
XX
DR WPI; 2002-691617/74.
XX
PT New potassium channel beta-subunit, K+betaM2, proteins and nucleic
PT acids, useful for diagnosing, treating and/or preventing e.g.
PT reproductive, neural, metabolic, endocrine, memory, neurodegenerative
PT disorders or diseases -
XX
PS Disclosure; Page 356; 366pp; English.
XX
CC The present invention relates to human potassium channel beta-subunit
CC (K+betaM2) proteins and polynucleotides encoding such proteins. The
CC K+betaM2 sequences are useful for diagnosing, treating and/or preventing
CC reproductive disorders, neural disorders, disorders related to aberrant
CC potassium regulation or hyper potassium channel activity, metabolic
CC disorders (e.g. premature puberty), endocrine disorders (e.g. aberrant
CC growth hormone synthesis and/or secretion), memory disorder, disorders
CC of the testis (e.g. spermatogenesis), neuroendocrine condition related
CC to aberrant thyroid hormone release, renal disease or disorders (e.g.
CC nephritis), disorders related to aberrant higher brain function (e.g.
CC learning deficiencies), neurodegenerative diseases (e.g. Alzheimer's
CC disease), proliferative disorders (e.g. carcinoid tumour) and disorders
CC involving excessive smooth muscle tone or excitability (e.g. asthma).
CC They may be used to modulate haemostatic or thrombolytic activity, to
CC treat or prevent blood coagulation diseases or disorders, blood platelet
CC diseases, wounds, autoimmune diseases, disorders or conditions (e.g.
CC rheumatoid arthritis), allergic reactions (e.g. asthma), organ rejection
CC or graft-versus-host disease, and hyperproliferative diseases. K+betaM2
CC sequences are also used in gene therapy. The present sequence is human
CC K+betaM2 protein fragment.
XX
SQ Sequence 103 AA;

Query Match 23.7%; Score 541; DB 23; Length 103;
Best Local Similarity 100.0%; Pred. No. 3.7e-46;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRY 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRY 60

Qy         85 ILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEI 127
              |||||||||||||||||||||||||||||||||||||||||||
Db         61 ILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEI 103
```

RESULT 8
ABB60184
ID ABB60184 standard; Protein; 228 AA.

XX
AC ABB60184;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 7344.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR N-PSDB; ABL04287.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 7344; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 228 AA;

Query Match 23.6%; Score 538.5; DB 22; Length 228;
Best Local Similarity 44.3%; Pred. No. 2.2e-45;
Matches 116; Conservative 44; Mismatches 61; Indels 41; Gaps 7;

```
Qy         24 PEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFR 83
              ||::||||||  | |  :||:    :|| ::|   ||:   ||||||||:|:|||| |||
Db          2 PEIIELNVGGVSYTTTLATLLQDKSTLLAELFGEGRDS---LAKDSKGRYFLDRDGVLFR 58

Qy         84 YILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDAS 143
```

```
              ||||:|||: : ||: | |: || ||||:|:|  ::: :  :
Db         59 YILDFLRDKALHLPEGFRERQRLLREAEHFKLTAMLECIRSER----------------- 101

Qy        144 QGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKE 203
                | |  ||          | ||:|||||   |::| || |||:: ||||||::  :|
Db        102 ---DAR--PP----------GCITIGYRGSFQFGKDGLADVKFRKLSRILVCGRVAQCRE 146

Qy        204 VFGETLNESRDPDR-APERYTSRFYLKFKHLERAFDMLSECGFHMV-ACNSSVTASFINQ 261
              |||:|||||||||    :||||||:||  ::|:||| | : |: |  :| |    |
Db        147 VFGDTLNESRDPDHGGTDRYTSRFFLKHCYIEQAFDNLHDHGYRMAGSCGSGTAGSAAEP 206

Qy        262 Y----TDDKIWSSYTEYVFYRE 279
                    |::  |: | |:|| |:
Db        207 KPGVDTEENRWNHYNEFVFIRD 228


RESULT 9
ABJ10887
ID   ABJ10887 standard; Protein; 228 AA.
XX
AC   ABJ10887;
XX
DT   05-DEC-2002  (first entry)
XX
DE   K+beta M6 related protein SEQ ID No 3.
XX
KW   Cytostatic; cardiant; neuroprotective; immunomodulator; antimigraine;
KW   sedative; gynaecological;; potassium channel beta subunit; K+betaM6;
KW   gastrointestinal; reproductive; neural; sleep; low DNA repair capacity;
KW   hyperpotassium channel activity; cardiovascular; melatonin synthesis;
KW   mammary cancer tumourigenesis; pineal gland associated disorder;
KW   pulmonary disorder; immune disorder; NF-kB activity; migraine headache;
KW   low free-radical buffering capacity; delayed sleep phase syndrome;
KW   circadian cycle; melatonin secretion; cancer.
XX
OS   Drosophila melanogaster.
XX
PN   WO200270727-A2.
XX
PD   12-SEP-2002.
XX
PF   21-FEB-2002; 2002WO-US05674.
XX
PR   21-FEB-2001; 2001US-270132P.
PR   27-MAR-2001; 2001US-278953P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Feder J,  Lee L,  Chen J,  Jackson DG,  Ramanathan C,  Siemers N;
PI   Chang H;
XX
DR   WPI; 2002-713455/77.
XX
PT   New polynucleotide encoding human potassium channel beta subunit
PT   polypeptide, useful for diagnosing, preventing, treating or
PT   ameliorating e.g. cancer  -
XX
```

PS Disclosure; Fig 2; 332pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding a potassium
CC channel beta subunit (K+betaM6) polypeptide or its variants. The human
CC potassium beta subunit polynucleotide or polypeptide is useful for
CC diagnosing, preventing, treating or ameliorating a pathological condition
CC such as gastrointestinal, reproductive, neural, sleep, cardiovascular or
CC pulmonary disorders, a disorder related to hyperpotassium channel
CC activity, an immune disorder related to aberrant NF-kB activity, pineal
CC gland associated disorders, migraine headaches, disorders associated with
CC aberrant melatonin synthesis and/or release or with low DNA repair
CC capacities or low free-radical buffering capacity, delayed sleep phase
CC syndrome, aberrations in circadian cycle, mammary cancer tumourigenesis,
CC age related disorders associated with decreased melatonin secretion, or
CC cancer. This sequence represents a potassium channel beta subunit
CC (K+betaM6) related protein of the invention.
XX
SQ Sequence 228 AA;

Query Match 23.6%; Score 538.5; DB 23; Length 228;
Best Local Similarity 44.3%; Pred. No. 2.2e-45;
Matches 116; Conservative 44; Mismatches 61; Indels 41; Gaps 7;

```
Qy         24 PEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFR 83
              ||::|||||| | |  :||:    :|| ::|   ||:   ||||||||:|:|||| |||
Db          2 PEIIELNVGGVSYTTTLATLLQDKSTLLAELFGEGRDS---LAKDSKGRYFLDRDGVLFR 58

Qy         84 YILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDAS 143
              ||||:|||: : ||: | |: || ||||:|:|  ::: :  :
Db         59 YILDFLRDKALHLPEGFRERQRLLREAEHFKLTAMLECIRSER----------------- 101

Qy        144 QGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKE 203
                 | |  ||          | ||:|||||   |::| || |||:: |||||||::  :|
Db        102 ---DAR--PP----------GCITIGYRGSFQFGKDGLADVKFRKLSRILVCGRVAQCRE 146

Qy        204 VFGETLNESRDPDR-APERYTSRFYLKFKHLERAFDMLSECGFHMV-ACNSSVTASFINQ 261
              |||:||||||||    :|||||||:||  ::|:||| | : |: |  :| |    |
Db        147 VFGDTLNESRDPDHGGTDRYTSRFFLKHCYIEQAFDNLHDHGYRMAGSCGSGTAGSAAEP 206

Qy        262 Y----TDDKIWSSYTEYVFYRE 279
                   |::  |: | |:|| |:
Db        207 KPGVDTEENRWNHYNEFVFIRD 228
```

RESULT 10
ABJ10893
ID ABJ10893 standard; Protein; 101 AA.
XX
AC ABJ10893;
XX
DT 05-DEC-2002 (first entry)
XX
DE K+beta M6 related protein SEQ ID No 13.
XX
KW Cytostatic; cardiant; neuroprotective; immunomodulator; antimigraine;
KW sedative; gynaecological;; potassium channel beta subunit; K+betaM6;
KW gastrointestinal; reproductive; neural; sleep; low DNA repair capacity;

KW hyperpotassium channel activity; cardiovascular; melatonin synthesis;
KW mammary cancer tumourigenesis; pineal gland associated disorder;
KW pulmonary disorder; immune disorder; NF-kB activity; migraine headache;
KW low free-radical buffering capacity; delayed sleep phase syndrome;
KW circadian cycle; melatonin secretion; cancer.
XX
OS Homo sapiens.
XX
PN WO200270727-A2.
XX
PD 12-SEP-2002.
XX
PF 21-FEB-2002; 2002WO-US05674.
XX
PR 21-FEB-2001; 2001US-270132P.
PR 27-MAR-2001; 2001US-278953P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Feder J, Lee L, Chen J, Jackson DG, Ramanathan C, Siemers N;
PI Chang H;
XX
DR WPI; 2002-713455/77.
XX
PT New polynucleotide encoding human potassium channel beta subunit
PT polypeptide, useful for diagnosing, preventing, treating or
PT ameliorating e.g. cancer -
XX
PS Disclosure; Fig 1; 332pp; English.
XX
CC The invention relates to an isolated polynucleotide encoding a potassium
CC channel beta subunit (K+betaM6) polypeptide or its variants. The human
CC potassium beta subunit polynucleotide or polypeptide is useful for
CC diagnosing, preventing, treating or ameliorating a pathological condition
CC such as gastrointestinal, reproductive, neural, sleep, cardiovascular or
CC pulmonary disorders, a disorder related to hyperpotassium channel
CC activity, an immune disorder related to aberrant NF-kB activity, pineal
CC gland associated disorders, migraine headaches, disorders associated with
CC aberrant melatonin synthesis and/or release or with low DNA repair
CC capacities or low free-radical buffering capacity, delayed sleep phase
CC syndrome, aberrations in circadian cycle, mammary cancer tumourigenesis,
CC age related disorders associated with decreased melatonin secretion, or
CC cancer. This sequence represents a potassium channel beta subunit
CC (K+betaM6) related protein of the invention.
XX
SQ Sequence 101 AA;

Query Match 16.1%; Score 367; DB 23; Length 101;
Best Local Similarity 68.4%; Pred. No. 1.1e-28;
Matches 67; Conservative 19; Mismatches 10; Indels 2; Gaps 1;

```
Qy         25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRY 84
              ::|||||||||| ||  |::|:| ||||:||: ::    :||:||||||:|||||||||
Db          1 DIVELNVGGQVYVTRRCTVVSVPDSLLWRMFTQQQ--PQELARDSKGRFFLDRDGFLFRY 58

Qy         85 ILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLL 122
              ||||||| |:||||:|||: ||:|||||:||:||: |
```

```
Db         59 ILDYLRDLQLVLPDYFPERSRLQREAEYFELPELVRRL 96

RESULT 11
AAM25877
ID   AAM25877 standard; Protein; 272 AA.
XX
AC   AAM25877;
XX
DT   16-OCT-2001  (first entry)
XX
DE   Human protein sequence SEQ ID NO:1392.
XX
KW   Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW   antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW   antibacterial; endocrine; cardiant; central nervous system; virucide;
KW   anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW   antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
KW   dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
KW   neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW   immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW   antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW   cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW   genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW   thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW   allergic rhinitis; diabetes; multiple sclerosis; depression;
KW   Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW   neurological disorder.
XX
OS   Homo sapiens.
XX
PN   WO200153455-A2.
XX
PD   26-JUL-2001.
XX
PF   22-DEC-2000; 2000WO-US35017.
XX
PR   23-DEC-1999;   99US-0471275.
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-457603/49.
DR   N-PSDB; AAH99818.
XX
PT   Isolated human polynucleotides encoding polypeptides, useful for the
PT   treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
XX
PS   Claim 20; Page 285; 1217pp; English.
XX
CC   AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC   AAM25963. The proteins can have activities based on the tissues and
CC   cells they are expressed in, such as: antiinflammatory; antirheumatic;
CC   antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
```

CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;
CC antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production, The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.
XX
SQ Sequence 272 AA;

Query Match 10.2%; Score 232; DB 22; Length 272;
Best Local Similarity 42.6%; Pred. No. 1.9e-14;
Matches 52; Conservative 23; Mismatches 39; Indels 8; Gaps 2;

```
Qy         12 PREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKG 71
                 |  |  |:     : : |||||::| |  :|| | | |:|  ||| |  |     :||:|
Db         17 PATQSPAM----SDPITLNVGGKLYTTSLATLTSFPDSMLGAMFSGKMPT----KRDSQG 68

Qy         72 RFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSP 131
                |||||| :|||||::||   : ||: | | | |:|||:::|:  |:: |   |:: |
Db         69 NCFIDRDGKVFRYILNFLRTSHLDLPEDFQEMGLLRREADFYQVQPLIEALQEKEVELSK 128

Qy        132 DE 133
               |
Db        129 AE 130
```

RESULT 12
ABP69573
ID ABP69573 standard; Protein; 290 AA.
XX
AC ABP69573;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human polypeptide SEQ ID NO 1620.
XX
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.
XX
OS Homo sapiens.

XX
PN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US05095.
XX
PR 05-MAR-2001; 2001US-0799451.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2002-759812/82.
DR N-PSDB; ABZ11790.
XX
PT New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or
PT platelet or coagulation disorders -
XX
PS Claim 9; SEQ ID NO 1620; 1012pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences
CC (ABZ11119-ABZ12066) or their mature protein coding portion, active domain
CC coding protein or complementary sequences. The polynucleotides are useful
CC for identifying expressed genes or for physical mapping of human genome.
CC The encoded polypeptides (ABP68902-ABP69849) are useful as molecular
CC weight markers, as a food supplement, for generating antibodies, in
CC medical imaging, screening and diagnostic assays and for treating
CC cell-proliferative disorders (cancer), neurodegenerative diseases
CC (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple
CC sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid
CC disorders, platelet or coagulation disorders, wound, burns, incision,
CC ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal,
CC parasitic), arthritis, etc.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 290 AA;

Query Match 10.1%; Score 231; DB 23; Length 290;
Best Local Similarity 45.8%; Pred. No. 2.7e-14;
Matches 49; Conservative 21; Mismatches 33; Indels 4; Gaps 1;

```
Qy         27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYIL 86
              : |||||::| |  :|| | | |:|  ||| |  |     :||:|  |||||| :|||||
Db          5 ITLNVGGKLYTTSLATLTSFPDSMLGAMFSGKMPT----KRDSQGNCFIDRDGKVFRYIL 60

Qy         87 DYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDE 133
              ::||   : ||: | | | |:|||:::|:  |:: |   |:: |  |
Db         61 NFLRTSHLDLPEDFQEMGLLRREADFYQVQPLIEALQEKEVELSKAE 107
```

RESULT 13
AAE10329
ID   AAE10329 standard; Protein; 339 AA.
XX
AC   AAE10329;
XX
DT   10-DEC-2001 (first entry)
XX
DE   Human transporter and ion channel-6 (TRICH-6) protein.
XX
KW   Human; transporter and ion channel; TRICH-6; therapy; akinesia; cardiant;
KW   neurological disorder; immune disorder; allergy; nootropic; dementia;
KW   AIDS; Acquired Immune Deficiency Syndrome; amyotrophic lateral sclerosis;
KW   cystic fibrosis; Alzheimer's disease; depression; epilepsy; scleroderma;
KW   cardiomyopathy; muscular dystrophy; Crohn's disease; multiple sclerosis;
KW   rheumatoid arthritis; cancer; anaemia; asthma; trauma; haemodialysis;
KW   gastritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..32
FT   /label= Signal_peptide
FT   Protein   33..339
FT   /label= Mature_TRICH_6_protein
XX
PN   WO200162923-A2.
XX
PD   30-AUG-2001.
XX
PF   23-FEB-2001; 2001WO-US05942.
XX
PR   25-FEB-2000; 2000US-0184866.
PR   02-MAR-2000; 2000US-0187947.
PR   09-MAR-2000; 2000US-0188333.
PR   17-MAR-2000; 2000US-0190230.
PR   24-MAR-2000; 2000US-0192077.
PR   30-MAR-2000; 2000US-0193500.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Yue H, Tang YT, Lal P, Policky JL, Nguyen DB, Au-Young J, Yao MG;
PI   Khan FA, Walia NK, Gandhi AR, Tribouley CM, Patterson C;
PI   Thornton M, Greene BD, Hernandez R, Borowsky ML, Sanjanwala MS;
XX
DR   WPI; 2001-582050/65.
DR   N-PSDB; AAD17473.
XX
PT   Thirteen human transporters and ion channels (referred to as TRICH-1 to
PT   TRICH-13), useful in the diagnosis, treatment and prevention of
PT   transport (e.g. akinesia), neurological, muscle or immunological
PT   disorders (e.g. allergies) -
XX
PS   Claim 1; Page 111; 131pp; English.
XX
CC   The present sequence is human transporters and ion channels

```
CC   (TRICH-6) protein. The TRICH DNA, protein and their agonist and
CC   antagonists are useful in the diagnosis, treatment and prevention of
CC   transport disorders (akinesia, amyotrophic lateral sclerosis, cystic
CC   fibrosis), neurological (Alzheimer's disease, dementia, depression,
CC   epilepsy), muscle (e.g. cardiomyopathy, Becker's muscular dystrophy) or
CC   immunological disorders (e.g. allergies, acquired immunodeficiency
CC   syndrome (AIDS), Crohn's disease, rheumatoid arthritis, scleroderma,
CC   multiple sclerosis), viral, bacterial, parasitic, protozoal and
CC   helminthic disorders, cancer, anaemia, asthma, trauma, haemodialysis,
CC   gastritis and inflammation.
XX
SQ   Sequence   339 AA;

  Query Match             10.1%;  Score 231;  DB 22;  Length 339;
  Best Local Similarity   45.8%;  Pred. No. 3.4e-14;
  Matches   49;  Conservative   21;  Mismatches   33;  Indels    4;  Gaps    1;

Qy         27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYIL 86
              : |||||::| |  :|| | | |:|  ||| |  |     :||:|  |||||| :|||||
Db          5 ITLNVGGKLYTTSLATLTSFPDSMLGAMFSGKMPT----KRDSQGNCFIDRDGKVFRYIL 60

Qy         87 DYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDE 133
              ::||   : ||: | | | |:|||:::|:  |:: |   |:: |  |
Db         61 NFLRTSHLDLPEDFQEMGLLRREADFYQVQPLIEALQEKEVELSKAE 107


RESULT 14
AAB41802
ID   AAB41802 standard; Protein; 283 AA.
XX
AC   AAB41802;
XX
DT   08-FEB-2001  (first entry)
XX
DE   Human ORFX ORF1566 polypeptide sequence SEQ ID NO:3132.
XX
KW   Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW   vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW   anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW   immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW   hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW   antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW   antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW   neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW   cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW   cholesterol ester storage; systemic lupus erythematosus; infection;
KW   severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW   allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW   bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW   thrombosis; contraceptive.
XX
OS   Homo sapiens.
XX
PN   WO200058473-A2.
XX
PD   05-OCT-2000.
XX
```

PF 31-MAR-2000; 2000WO-US08621.
XX
PR 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2000-602362/57.
DR N-PSDB; AAC76011.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
PS Claim 11; Page 2349-2350; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antithyroid; and antianaemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ Sequence 283 AA;

Query Match 9.2%; Score 210.5; DB 21; Length 283;
Best Local Similarity 28.3%; Pred. No. 2.9e-12;
Matches 80; Conservative 41; Mismatches 89; Indels 73; Gaps 13;

```
Qy         15 QGSAVPNSFPE---VVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDS-K 70
              ||  :|    :    | ::||| :| :  :||   | | : ::|    |    :  || |
Db         43 QGIPLPAQLTKSNAPVHIDVGGHMYTSSLATLTKYPESRIGRLF----DGTEPIVLDSLK 98

Qy         71 GRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQS 130
                :|||||| :|||||::||  ::::|| | :   |  ||:|||| :  ||  :  ||
Db         99 QHYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQLQPM--LLEMERWKQ- 155

Qy        131 PDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVP 190
```

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                     |   |  :| |                :  | :  ||
Db        156 ----------DRETGRFSRPCE-------------CLVVRVAPDLGE---------- 179

Qy        191 RILVCGRISLAKEVFGE-------TLNESRDPDRAPERYTSRFYLK-FKHLE--RAFDML 240
              || : |  || :||| |       ::|   : |     :  || |  : ||   :  : |
Db        180 RITLSGDKSLIEEVFPEIGDVMCNSVNAGWNHD---STHVIRFPLNGYCHLNSVQVLERL 236

Qy        241 SECGFHMV-ACNSSVTASFINQYTDDKIWSSYTEYVFYREPSR 282
               : || :| :|   | :            | ::|||  ||  |
Db        237 QQRGFEIVGSCGGGVDS------------SQFSEYVLRRELRR 267
```

RESULT 15
AAY34125
ID AAY34125 standard; Protein; 256 AA.
XX
AC AAY34125;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human potassium channel K+Hnov27.
XX
KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
KW cardiovascular disorder; CNS disorder; renal disorder.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Misc-difference 15
FT   /label= Ile, Asn
FT   /note= "Encoded by AWC"
XX
PN WO9943696-A1.
XX
PD 02-SEP-1999.
XX
PF 22-FEB-1999; 99WO-US03826.
XX
PR 19-JAN-1999; 99US-0116448.
PR 25-FEB-1998; 98US-0076687.
PR 07-AUG-1998; 98US-0095836.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Curran ME, Hu P, Miller AP, Rutter M, Wang J;
XX
DR WPI; 1999-527591/44.
DR N-PSDB; AAZ11903.
XX
PT New nucleic acids encoding mammalian K+Hnov potassium channel
PT proteins, useful for the diagnosis and treatment of episodic ataxia
PT with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome
XX
PS Claim 3; Page 66; 112pp; English.
XX
CC This sequence represents the human K+Hnov27 potassium channel.
CC K+Hnov proteins have a high degree of homology to known potassium

```
CC   channels and may be alpha subunits, which form the functional channel,
CC   or accessory subunits that act to modulate the channel activity.
CC   K+Hnov27 is a potassium channel modulatory subunit. The gene's
CC   chromosomal location is 18q12, determined via PCR
CC   chromosomal localisation. K+Hnov cDNAs were isolated
CC   by extension of expressed sequence tags (ESTs) which were
CC   related but not identical to known human potassium channels. Potential
CC   polymorphisms detected as sequence variants between multiple
CC   independent clones. Potassium channels have critical roles in various
CC   cell types and biochemical pathways. Defective potassium channels are
CC   known to cause four human diseases: episodic ataxia with myokymia;
CC   cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
CC   As potassium channels are critical components of virtually all cells,
CC   it is likely that abnormal potassium channels are also implicated in
CC   certain renal, cardiovascular and central nervous system (CNS) disorders.
CC   Nucleotides encoding K+Hnov proteins may be used for identifying
CC   homologous or related proteins and the DNA sequences encoding them. They
CC   may be used to produce compositions that modulate the expression and
CC   function of the K+Hnov protein and in studying the biochemical pathways
CC   associated with it. They may also be used for the recombinant production
CC   of K+Hnov protein in fermentation cultures. Additionally, such
CC   nucleotides may be used in gene therapy protocols for the treatment
CC   of diseases associated with abnormal potassium channels.
XX
SQ   Sequence   256 AA;

  Query Match             9.2%;  Score 210;  DB 20;  Length 256;
  Best Local Similarity   28.7%;  Pred. No. 2.8e-12;
  Matches   77;  Conservative   39;  Mismatches   82;  Indels   70;  Gaps   12;

Qy         27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDS-KGRFFIDRDGFLFRYI 85
              | ::||| :| :  :||   | | : ::|    |    :  || |  :|||||| :||||
Db         32 VHIDVGGHMYTSSLATLTKYPESRIGRLF----DGTEPIVLDSLKQHYFIDRDGQMFRYI 87

Qy         86 LDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQG 145
              |::||  ::::|| | :   |  ||:||||  :  ||  :  ||           |   |
Db         88 LNFLRTSKLLIPDDFKDYTLLYEEAKYFQLQPM--LLEMERWKQ----------DRETG 134

Qy        146 SDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVF 205
             :| |                :  | :  ||             || : |  || :|||
Db        135 RFSRPCE-------------CLVVRVAPDLGE-----------RITLSGDKSLIEEVF 168

Qy        206 GE-------TLNESRDPDRAPERYTSRFYLK-FKHLE--RAFDMLSECGFHMV-ACNSSV 254
               |       ::|   : |     :  || |  : ||   :  : | : || :| :|   |
Db        169 PEIGDVMCNSVNAGWNHD---STHVIRFPLNGYCHLNSVQVLERLQQRGFEIVGSCGGGV 225

Qy        255 TASFINQYTDDKIWSSYTEYVFYREPSR 282
             :            | ::|||  ||  |
Db        226 DS-----------SQFSEYVLRRELRR 241


Search completed: January 29, 2004, 02:52:25
Job time : 57 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 29, 2004, 02:51:31 ; Search time 23 Seconds
(without alignments)
787.350 Million cell updates/sec

Title: US-10-056-884A-2
Perfect score: 2284
Sequence: 1 MALSGNCSRYYPREQGSAVP.....DRFPERKHPWQSELLRKYHL 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	210	9.2	256	4	US-09-336-643A-14	Sequence 14, Appl
2	202.5	8.9	237	4	US-09-336-643A-25	Sequence 25, Appl
3	189	8.3	258	4	US-09-336-643A-12	Sequence 12, Appl
4	146.5	6.4	812	4	US-09-166-350-12	Sequence 12, Appl
5	133.5	5.8	389	4	US-09-336-643A-27	Sequence 27, Appl
6	106	4.6	646	4	US-09-336-643A-10	Sequence 10, Appl
7	100.5	4.4	162	2	US-08-606-143-44	Sequence 44, Appl
8	100	4.4	490	4	US-09-336-643A-6	Sequence 6, Appli
9	95.5	4.2	499	4	US-09-336-643A-8	Sequence 8, Appli
10	95	4.2	1384	3	US-08-976-255-11	Sequence 11, Appl
11	94.5	4.1	3287	2	US-08-477-451-7	Sequence 7, Appli

12	92.5	4.0	848	3	US-08-976-255-10	Sequence 10, Appl
13	92	4.0	393	4	US-09-252-991A-25633	Sequence 25633, A
14	92	4.0	636	4	US-09-142-791A-2	Sequence 2, Appli
15	92	4.0	636	4	US-09-178-109-4	Sequence 4, Appli
16	92	4.0	655	4	US-09-142-791A-4	Sequence 4, Appli
17	92	4.0	655	4	US-09-178-109-2	Sequence 2, Appli
18	92	4.0	768	2	US-08-408-519-2	Sequence 2, Appli
19	92	4.0	768	5	PCT-US95-03552-2	Sequence 2, Appli
20	91.5	4.0	664	3	US-09-295-186-17	Sequence 17, Appl
21	91	4.0	580	3	US-08-482-677-10	Sequence 10, Appl
22	90.5	4.0	352	4	US-09-328-352-8196	Sequence 8196, Ap
23	89.5	3.9	2289	3	US-09-051-019-2	Sequence 2, Appli
24	87.5	3.8	1065	4	US-09-221-013A-10	Sequence 10, Appl
25	86.5	3.8	601	4	US-09-336-643A-4	Sequence 4, Appli
26	86.5	3.8	685	3	US-08-960-048-7	Sequence 7, Appli
27	86.5	3.8	685	4	US-09-838-586-7	Sequence 7, Appli
28	86.5	3.8	1317	3	US-09-083-521-7	Sequence 7, Appli
29	86	3.8	296	4	US-07-757-022B-70	Sequence 70, Appl
30	86	3.8	528	2	US-08-527-152-2	Sequence 2, Appli
31	86	3.8	875	4	US-09-328-352-4884	Sequence 4884, Ap
32	84.5	3.7	1471	3	US-08-755-587-188	Sequence 188, App
33	84	3.7	190	2	US-08-606-143-37	Sequence 37, Appl
34	84	3.7	208	2	US-08-606-143-40	Sequence 40, Appl
35	84	3.7	448	1	US-08-295-411-3	Sequence 3, Appli
36	84	3.7	448	2	US-08-955-471-3	Sequence 3, Appli
37	84	3.7	448	5	PCT-US92-10242-3	Sequence 3, Appli
38	84	3.7	636	4	US-09-142-791A-6	Sequence 6, Appli
39	84	3.7	881	3	US-08-960-048-8	Sequence 8, Appli
40	84	3.7	881	4	US-09-838-586-8	Sequence 8, Appli
41	83.5	3.7	159	2	US-08-606-143-45	Sequence 45, Appl
42	83.5	3.7	339	1	US-08-248-629A-5	Sequence 5, Appli
43	83.5	3.7	339	1	US-08-451-932-5	Sequence 5, Appli
44	83.5	3.7	339	1	US-08-452-260-5	Sequence 5, Appli
45	83.5	3.7	339	1	US-08-326-785-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-336-643A-14
; Sequence 14, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19

```
;  PRIOR APPLICATION NUMBER: PCT/US99/03826
;  PRIOR FILING DATE: 1999-02-22
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: H. sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(256)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-336-643A-14

  Query Match             9.2%;  Score 210;  DB 4;  Length 256;
  Best Local Similarity   28.7%;  Pred. No. 2.2e-13;
  Matches   77;  Conservative   39;  Mismatches   82;  Indels   70;  Gaps   12;

Qy         27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDS-KGRFFIDRDGFLFRYI 85
              | ::||| :| :  :||   | | : ::|    |    :  || |  :|||||| :|||| 
Db         32 VHIDVGGHMYTSSLATLTKYPESRIGRLF----DGTEPIVLDSLKQHYFIDRDGQMFRYI 87

Qy         86 LDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQG 145
              |::||  ::::|| | :   |  ||:||||  :  ||  :  ||           |   |
Db         88 LNFLRTSKLLIPDDFKDYTLLYEEAKYFQLQPM--LLEMERWKQ-----------DRETG 134

Qy        146 SDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVF 205
               :| |                :  | :  ||             || : |  || :|||
Db        135 RFSRPCE--------------CLVVRVAPDLGE-----------RITLSGDKSLIEEVF 168

Qy        206 GE-------TLNESRDPDRAPERYTSRFYLK-FKHLE--RAFDMLSECGFHMV-ACNSSV 254
               |       ::|   : |     :  || |  : ||   :  : | : || :| :|   |
Db        169 PEIGDVMCNSVNAGWNHD---STHVIRFPLNGYCHLNSVQVLERLQQRGFEIVGSCGGGV 225

Qy        255 TASFINQYTDDKIWSSYTEYVFYREPSR 282
               :            | ::|||  ||  |
Db        226 DS------------SQFSEYVLRRELRR 241


RESULT 2
US-09-336-643A-25
; Sequence 25, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
;  APPLICANT: Miller, Andrew P.
;  APPLICANT:  Curran, Mark Edward
;  APPLICANT:  Hu, Ping
;  APPLICANT:  Rutter, Marc
;  APPLICANT:  Wang, Jian-Wang
;  TITLE OF INVENTION: No. 6399761el Human Potassium Channels
;  FILE REFERENCE: SEQ-15P
;  CURRENT APPLICATION NUMBER: US/09/336,643A
;  CURRENT FILING DATE:  1999-06-18
;  PRIOR APPLICATION NUMBER: 60/076,687
;  PRIOR FILING DATE: 1998-08-07
;  PRIOR APPLICATION NUMBER: 60/116,448
;  PRIOR FILING DATE: 1999-01-19
```

```
;  PRIOR APPLICATION NUMBER: PCT/US99/03826
;  PRIOR FILING DATE: 1999-02-22
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
;   LENGTH: 237
;   TYPE: PRT
;   ORGANISM: H. sapiens
US-09-336-643A-25

  Query Match              8.9%;  Score 202.5;  DB 4;  Length 237;
  Best Local Similarity   39.0%;  Pred. No. 1.2e-12;
  Matches   48;  Conservative   22;  Mismatches   44;  Indels    9;  Gaps    2;

Qy         27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYIL 86
              | ||||| :| |  :||   | |:|  ||     |    |:| :| :|||||| ||||:|
Db         14 VTLNVGGHLYTTSLTTLTRYPDSMLGAMFGGDFPT----ARDPQGNYFIDRDGPLFRYVL 69

Qy         87 DYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQGS 146
              ::||  :: ||  | |   |::||:::|:  |:: |   :     |      ||:  : |
Db         70 NFLRTSELTLPLDFKEFDLLRKEADFYQIEPLIQCLNDPKPLYPMD-----TFEEVVELS 124

Qy        147 DTR 149
               ||
Db        125 STR 127


RESULT 3
US-09-336-643A-12
; Sequence 12, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
;  APPLICANT: Miller, Andrew P.
;  APPLICANT:  Curran, Mark Edward
;  APPLICANT:  Hu, Ping
;  APPLICANT:  Rutter, Marc
;  APPLICANT:  Wang, Jian-Wang
;  TITLE OF INVENTION: No. 6399761el Human Potassium Channels
;  FILE REFERENCE: SEQ-15P
;  CURRENT APPLICATION NUMBER: US/09/336,643A
;  CURRENT FILING DATE:  1999-06-18
;  PRIOR APPLICATION NUMBER: 60/076,687
;  PRIOR FILING DATE: 1998-08-07
;  PRIOR APPLICATION NUMBER: 60/116,448
;  PRIOR FILING DATE: 1999-01-19
;  PRIOR APPLICATION NUMBER: PCT/US99/03826
;  PRIOR FILING DATE: 1999-02-22
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 258
;   TYPE: PRT
;   ORGANISM: H. sapiens
US-09-336-643A-12

  Query Match              8.3%;  Score 189;  DB 4;  Length 258;
  Best Local Similarity   34.7%;  Pred. No. 3.2e-11;
```

```
  Matches   51;  Conservative   24;  Mismatches   40;  Indels   32;  Gaps    6;

Qy         14 EQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLL-----WKMFSPKRDTANDLAKD 68
              :||    |    :: ||||| :| |:  ||   | : |      |:  |          |
Db         25 DQGK---NCKSTLMTLNVGGYLYITQKQTLTKYPDTFLEGIVNGKILCP---------FD 72

Qy         69 SKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIK 128
              : | :|||||| |||::|::||: :::||: | |   | :|||:|||  |      :|:|
Db         73 ADGHYFIDRDGLLFRHVLNFLRNGELLLPEGFRENQLLAQEAEFFQLKGLA-----EEVK 127

Qy        129 Q-------SPDEFCH---SDFEDASQG 145
                     :| |      :|  | |||
Db        128 SRWEKEQLTPRETTFLEITDNHDRSQG 154


RESULT 4
US-09-166-350-12
; Sequence 12, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew
;  APPLICANT: Chen, Yao
;  APPLICANT: Stockert, Elisabeth
;  APPLICANT: Old, Lloyd
;  APPLICANT: Jager, Elke
;  APPLICANT: Knuth, Alex
;  TITLE OF INVENTION: Renal Cancer Associated Antigens and
;  TITLE OF INVENTION: Uses Therefor
;  FILE REFERENCE: L0461/7051
;  CURRENT APPLICATION NUMBER: US/09/166,350A
;  CURRENT FILING DATE: 1998-10-05
;  EARLIER APPLICATION NUMBER: US 09/166,350
;  EARLIER FILING DATE: 1998-10-05
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
;   LENGTH: 812
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-166-350-12

  Query Match              6.4%;  Score 146.5;  DB 4;  Length 812;
  Best Local Similarity   32.8%;  Pred. No. 4.5e-06;
  Matches   43;  Conservative   24;  Mismatches   43;  Indels   21;  Gaps    5;

Qy          5 GNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTAND 64
              |:|  :     ||       |:|:|||||  : |   ||: || |    : | :  |
Db          4 GHCGSFPAAAAGSG------EIVQLNVGGTRFSTSRQTLMWIPDSFFSSLLSGRIST--- 54

Qy         65 LAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKG----RLKREAEYFQLPDLV- 119
               :|  |  |||||   |  ||::|| ::: |      :|     |: |||:: :  ||
Db         55 -LRDETGAIFIDRDPAAFAPILNFLRTKELDL------RGVSINVLRHEAEFYGITPLVR 107

Qy        120 KLLTPDEIKQS 130
              :||  :|:::|
Db        108 RLLLCEELERS 118
```

RESULT 5
US-09-336-643A-27
; Sequence 27, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 389
;   TYPE: PRT
;   ORGANISM: H. sapiens
US-09-336-643A-27

  Query Match   5.8%; Score 133.5; DB 4; Length 389;
  Best Local Similarity   33.3%; Pred. No. 3.3e-05;
  Matches   45; Conservative   17; Mismatches   48; Indels   25; Gaps   5;

```
Qy          29 LNVGGQVYFTRHSTLIS-IPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYILD 87
               |||||: : |  |||::  | |:|  ||  |    |   :| :| | |||    |  ||:
Db          93 LNVGGRYFTTTRSTLVNKEPDSMLAHMFKDKGVWGN--KQDHRGAFLIDRSPEYFEPILN 150

Qy          88 YLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQGSD 147
               |||  |::: |     | |: || :| :  |:: |                 | | : |
Db         151 YLRHGQLIVNDGINLLGVLE-EARFFGIDSLIEHL----------------EVAIKNSQ 192

Qy         148 TRICPPSSLLPADRK 162
                   ||    |  ||
Db         193 ----PPEDHSPISRK 203
```

RESULT 6
US-09-336-643A-10
; Sequence 10, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels

```
;  FILE REFERENCE: SEQ-15P
;  CURRENT APPLICATION NUMBER: US/09/336,643A
;  CURRENT FILING DATE:  1999-06-18
;  PRIOR APPLICATION NUMBER: 60/076,687
;  PRIOR FILING DATE: 1998-08-07
;  PRIOR APPLICATION NUMBER: 60/116,448
;  PRIOR FILING DATE: 1999-01-19
;  PRIOR APPLICATION NUMBER: PCT/US99/03826
;  PRIOR FILING DATE: 1999-02-22
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 646
;   TYPE: PRT
;   ORGANISM: H. sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(646)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-09-336-643A-10

  Query Match             4.6%;  Score 106;  DB 4;  Length 646;
  Best Local Similarity   21.8%;  Pred. No. 0.049;
  Matches   65;  Conservative   36;  Mismatches   87;  Indels  110;  Gaps   13;

Qy         26 VVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYI 85
              |: :|| |: : |  :||   | :||    | :::   |      | :| |||  :||::
Db         41 VLVVNVSGRRFETWKNTLDRYPDTLLG---SSEKEFFYDA---DSGEYFFDRDPDMFRHV 94

Qy         86 LDYLRDRQVVLPDHFPEKGRLKREAE----YFQLPDLVKLLTPDEIKQSPDEFCH--SDF 139
              |:: |  ::    | | :  ::   |    |  :|:||     :| :    |     ::
Db         95 LNFYRTGRL----HCPRQECIQAFDEELAFYGLVPELVGDCCLEEYRDRKKENAERLAED 150

Qy        140 EDASQGSDTRICPPSSLLPADRKW-------------------GFI-----------TVG 169
              |:| |  |    |  | |   | |                   ||            |:
Db        151 EEAEQAGDGPALPAGSSL-RQRLWRAFENPHTSTAALVFYYVTGFFIAVSVIANVVETIP 209

Qy        170 YRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFY-- 227
               |||             ||  |   ||                       ||:   |:
Db        210 CRGSA-----------RRSSREQPCG----------------------ERFPQAFFCM 234

Qy        228 -----LKF--KHLERAFDMLSECGF-------------------HMVACNSSVTASFI 259
                  | |  ::| | |   | | |                     :|  |  |: :|:
Db        235 DTACVLIFTGEYLLRLFAAPSRCRFLRSVMSLIDVVAILPYYIGLLVPKNDDVSGAFV 292


RESULT 7
US-08-606-143-44
; Sequence 44, Application US/08606143
; Patent No. 5856155
;  GENERAL INFORMATION:
;    APPLICANT:  Li, Min
;    TITLE OF INVENTION:  COMPOUNDS AND RELATED METHODS FOR
;    TITLE OF INVENTION:  MODULATING POTASSIUM ION CHANNELS AND ASSAYS FOR SUCH
;    TITLE OF INVENTION:  COMPOUNDS
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;       STREET:  Two Prudential Plaza, Suite 4900
;       CITY:  Chicago
;       STATE:  IL
;       COUNTRY:  USA
;       ZIP:  60601
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/606,143
;       FILING DATE:  23-FEB-1996
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kilyk Jr., John
;       REGISTRATION NUMBER:  30763
;       REFERENCE/DOCKET NUMBER:  71756
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (312) 616-5600
;       TELEFAX:  (312) 616-5700
;       TELEX:  25-3533
;  INFORMATION FOR SEQ ID NO:  44:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  162 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-606-143-44

  Query Match              4.4%;  Score 100.5;  DB 2;  Length 162;
  Best Local Similarity   26.9%;  Pred. No. 0.022;
  Matches   39;  Conservative   28;  Mismatches   61;  Indels   17;  Gaps    6;

Qy         25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRY 84
              ||: :|| |: : |  :||   | :||    | :::   |      | :| |||  :||:
Db          2 EVLVVNVSGRRFETWKNTLDRYPDTLLG---SSEKEFFYDA---ESGEYFFDRDPDMFRH 55

Qy         85 ILDYLRDRQVVLPDHFPEKGRLKREAE----YFQLPDLVKLLTPDEIKQSPDEFCH--SD 138
              :|:: |  ::    | | :  ::   |    |  :|:||     :| :    |     ::
Db         56 VLNFYRTGRL----HCPRQECIQAFDEELAFYGLVPELVGDCCLEEYRDRKKENAERLAE 111

Qy        139 FEDASQGSDTRICPPSSLLPADRKW 163
               |:| |  :    |  | |   | |
Db        112 DEEAEQAGEGPALPAGSSL-RQRLW 135


RESULT 8
US-09-336-643A-6
; Sequence 6, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
;  APPLICANT: Miller, Andrew P.
;  APPLICANT:  Curran, Mark Edward
;  APPLICANT:  Hu, Ping
```

```
;  APPLICANT:  Rutter, Marc
;  APPLICANT:  Wang, Jian-Wang
;  TITLE OF INVENTION: No. 6399761el Human Potassium Channels
;  FILE REFERENCE: SEQ-15P
;  CURRENT APPLICATION NUMBER: US/09/336,643A
;  CURRENT FILING DATE:  1999-06-18
;  PRIOR APPLICATION NUMBER: 60/076,687
;  PRIOR FILING DATE: 1998-08-07
;  PRIOR APPLICATION NUMBER: 60/116,448
;  PRIOR FILING DATE: 1999-01-19
;  PRIOR APPLICATION NUMBER: PCT/US99/03826
;  PRIOR FILING DATE: 1999-02-22
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 490
;   TYPE: PRT
;   ORGANISM: H. sapiens
US-09-336-643A-6

  Query Match              4.4%;  Score 100;  DB 4;  Length 490;
  Best Local Similarity   25.4%;  Pred. No. 0.13;
  Matches   35;  Conservative   28;  Mismatches   61;  Indels   14;  Gaps    5;

Qy         20 PNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTA-----NDLAKDSKGRFF 74
                 |    |:| |||||       |||:  ||: | |: :   : |     :| :   |  ::
Db         10 PGQDEELVNLNVGGFKQSVDQSTLLRFPHTRLGKLLTCHSEEAILELCDDYSVADK-EYY 68

Qy         75 IDRDGFLFRYILDYLRDRQVVLPDHFPEK---GRLKREAEYFQLPDL-VKLLTPDEIKQS 130
               ||:  ||||:|::    ::    |  |:       :| ||: : :| :     :  ::
Db         69 FDRNPSLFRYVLNFYYTGKL----HVMEELCVFSFCQEIEYWGINELFIDSCCSNRYQER 124

Qy        131 PDEFCHSDFEDASQGSDT 148
               :|    |::  |    |
Db        125 KEENHEKDWDQKSHDVST 142


RESULT 9
US-09-336-643A-8
; Sequence 8, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
;  APPLICANT: Miller, Andrew P.
;  APPLICANT:  Curran, Mark Edward
;  APPLICANT:  Hu, Ping
;  APPLICANT:  Rutter, Marc
;  APPLICANT:  Wang, Jian-Wang
;  TITLE OF INVENTION: No. 6399761el Human Potassium Channels
;  FILE REFERENCE: SEQ-15P
;  CURRENT APPLICATION NUMBER: US/09/336,643A
;  CURRENT FILING DATE:  1999-06-18
;  PRIOR APPLICATION NUMBER: 60/076,687
;  PRIOR FILING DATE: 1998-08-07
;  PRIOR APPLICATION NUMBER: 60/116,448
;  PRIOR FILING DATE: 1999-01-19
;  PRIOR APPLICATION NUMBER: PCT/US99/03826
;  PRIOR FILING DATE: 1999-02-22
```

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;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 499
;   TYPE: PRT
;   ORGANISM: H. sapiens
US-09-336-643A-8

  Query Match              4.2%;  Score 95.5;  DB 4;  Length 499;
  Best Local Similarity   23.5%;  Pred. No. 0.4;
  Matches   47;  Conservative   24;  Mismatches   72;  Indels   57;  Gaps    9;

Qy         15 QGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMF----------------SPK 58
              :|   | :  :   :||||  :      |   ||: | |:                  ||
Db         29 EGEGEPLALGDCFTVNVGGSRFVLSQQALSCFPHTRLGKLAVVVASYRRPGALAAVPSPL 88

Qy         59 R--DTANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKR-------- 108
                | || :  :    :| ||    |||:| | |  :: : :       |:
Db         89 ELCDDANPVDNE----YFFDRSSQAFRYVLHYYRTGRLHVMEQLCALSFLQEIQYWGIDE 144

Qy        109 -------EAEYFQLPDLVKLLTPDEIKQSPD-EFCHSDFEDASQGSDTRICP-------- 152
                    ||:  :| : |  |  | : | |  |   :| |||     ||
Db        145 LSIDSCCRDRYFRRKELSETL--DFKKDTEDQESQHESEQDFSQGP----CPTVRQKLWN 198

Qy        153 ----PSSLLPADRKWGFITV 168
                |  |   | | :| |::
Db        199 ILEKPGSSTAA-RIFGVISI 217


RESULT 10
US-08-976-255-11
; Sequence 11, Application US/08976255
; Patent No. 6136581
;  GENERAL INFORMATION:
;    APPLICANT:  Jono, Keith E.
;    APPLICANT:  Plowman, Gregory
;    TITLE OF INVENTION:  KINASE GENES AND USES
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/976,255
;      FILING DATE:  No. 6136581ember 21, 1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  60/031,675
;      FILING DATE:  No. 6136581ember 22, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  229/182
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1384 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Protein
US-08-976-255-11

  Query Match             4.2%;  Score 95;  DB 3;  Length 1384;
  Best Local Similarity   30.1%;  Pred. No. 2.1;
  Matches   46;  Conservative   20;  Mismatches   55;  Indels   32;  Gaps    8;

Qy        288 CDCCCKNGKGDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIK 347
              | || | | | || |     |          ||  ||  ||  ||      :  :  |:
Db         61 CLCCKKGGIGFKEFE-----NAEGEEYVADFSEQGSPAATVQNGPDVYVLPLTEVSLPMA 115

Qy        348 KGP---VQLIQQSEMRRKSDLLRI----------LTSGSRESNMSSKKKAVKE---KLSI 391
              | |   |||:: ::: | | || :          :  |   | :|| :  |||     |:
Db        116 KQPGRSVQLLKSTDVGRHS-LLYLKEIGRGWFGKVFLGEVNSGISSAQVVVKELQASASV 174

Qy        392 EEELEKCIQDFLKKKIPDRFPERKHPWQSELLR 424
              :|:::     ||::  | |    ||   | ||:
Db        175 QEQMQ-----FLEEVQPYR--ALKH---SNLLQ 197


RESULT 11
US-08-477-451-7
; Sequence 7, Application US/08477451
; Patent No. 5928865
;  GENERAL INFORMATION:
;    APPLICANT:  Covacci, Antonello
;    TITLE OF INVENTION:  Helicobacter Pylori Cagi Region
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Chiron Corporation
;      STREET:  4560 Horton Street
;      CITY:  Emeryville
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94608-2916
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;       APPLICATION NUMBER:  US/08/477,451
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McClung, Barbara G.
;       REGISTRATION NUMBER:  33,113
;       REFERENCE/DOCKET NUMBER:  0335.002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  510-601-2708
;       TELEFAX:  510-655-3542
;  INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3287 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-477-451-7

  Query Match             4.1%;  Score 94.5;  DB 2;  Length 3287;
  Best Local Similarity   20.8%;  Pred. No. 8.8;
  Matches   93;  Conservative   57;  Mismatches  170;  Indels  127;  Gaps   19;

Qy         42 TLISIPHSLLWKMFSPK---------RDTA--NDLAK---------------DSKGRFF- 74
              ||||:   ||   | |:         :|    ||| |               : | |||
Db       1896 TLISLGLFLLVFRFQPETIKKYIKDPKDLQFYNDLRKKNGWDKVYYSMMSVAEQKRRFFK 1955

Qy         75 ---IDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPD----------LVKL 121
                    :     : | |  | |        |: |:|    : :: |           ||
Db       1956 LSSACMNSIKILFFLIYSSDFQF-------ERKRMK---FFTRITDSYKKVVVTLGLVVT 2005

Qy        122 LTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQ 181
                |     || |        |::|   :|    :::              | | || :|
Db       2006 TNPLMAVASPTEGV-----TATKGLVIQIISVLAIV-------------GGCALGVKGI 2046

Qy        182 AD----------------AKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSR 225
              ||                |  : :  : | | |      ||  : |        :: | |
Db       2047 ADIWKISDDIKRGQATVFAYAQPIAMLAVAGGIIYLSTKFGFNIGEGGGASVDQQQETKR 2106

Qy        226 FYLKFKHLERAFDMLSECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFY-------- 277
               : :     | |       |  |:   |   |   :    : |:   :: |:
Db       2107 LFFESSLKSRCFQ------FVWVSKQRSQKRSTRKRKKHSQ-WACLYKFRFFQSDYQKFE 2159

Qy        278 REPSRWSPSHC---------DCCCKNGKG---------DKEGESGTSC--NDLSTSSCDS 317
              |: | :  |           ||     ||         : :| :|  |   | |:
Db       2160 RQESNFQRSQSRYYQRSFLRDCQSPKNKGFEALRSSYKNLKGGNGIECRITDQSSERLFY 2219

Qy        318 QSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEM--RRKS--DLLRILTSG- 372
                :    |:| :   : |:    ::      | :| :   |   || |  :||    ||
Db       2220 FQKHQHDQQTTLLSVIARRNKRNSMRVICFIGRIQFLSSFETYHRRVSQKNLLYDYMSGI 2279

Qy        373 --SRESNMSSKKKAVKEKLSIEEELEK 397
                 ||  ::||:   ::|| ||:|::|
Db       2280 SIKREVFVASKQADEQKKLIIEQEVQK 2306

RESULT 12
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US-08-976-255-10
; Sequence 10, Application US/08976255
; Patent No. 6136581
;  GENERAL INFORMATION:
;    APPLICANT:  Jono, Keith E.
;    APPLICANT:  Plowman, Gregory
;    TITLE OF INVENTION:  KINASE GENES AND USES
;    NUMBER OF SEQUENCES:  53
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/976,255
;      FILING DATE:  No. 6136581ember 21, 1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/031,675
;      FILING DATE:  No. 6136581ember 22, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  229/182
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  848 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Protein
US-08-976-255-10

  Query Match             4.0%;  Score 92.5;  DB 3;  Length 848;
  Best Local Similarity   28.8%;  Pred. No. 1.8;
  Matches   40;  Conservative   19;  Mismatches   53;  Indels   27;  Gaps    6;

Qy        288 CDCCCKNGKGDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIK 347
              | || | | | || |     |          ||  ||  ||  ||      :  :  |:
Db         61 CLCCKKGGIGFKEFE-----NAEGEEYVADFSEQGSPAATVQNGPDVYVLPLTEVSLPMA 115

Qy        348 KGP---VQLIQQSEMRRKSDLLRI----------LTSGSRESNMSSKKKAVKE---KLSI 391
              | |   |||:: ::: | | || :          :  |   | :|  :  |||     |:
Db        116 KQPGRSVQLLKSTDLGRHS-LLYLKEIGHGWFGKVFLGEVHSGVSGTQVVVKELKASASV 174
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Qy         392 EEELEKCIQDFLKKKIPDR 410
               :|:::     ||::  | |
Db         175 QEQMQ-----FLEEAQPYR 188


RESULT 13
US-09-252-991A-25633
; Sequence 25633, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 25633
;   LENGTH: 393
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25633

  Query Match             4.0%;  Score 92;  DB 4;  Length 393;
  Best Local Similarity   22.4%;  Pred. No. 0.64;
  Matches   44;  Conservative   20;  Mismatches   76;  Indels   56;  Gaps    7;

Qy         234 ERAFDMLSECGFHMVA-CNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCC- 291
               ||       ||   |: | || | |                          ||  :   ||
Db           3 ERCRKNCCACGKRCVSPCCSSPTPS----------------------RRRWWWATASCCS 40

Qy         292 --CKNGKGDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKG 349
                 : | | |   : : |  |: | |  : :||    |  |   ||  |
Db          41 RRTRGGSGPKCTATRSGCTALAASRCKPRRDAS----TACCS--TRAAN---------- 83

Qy         350 PVQLIQQSEMRRKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPD 409
                       ||:    |  ||      :  : :::     : || |  ::  |:  :
Db          84 ----------RRRP---RPSTSPISGWPIEQRNRSMSRVTRVREEYEVQLEPLLEVSLER 130

Qy         410 RFPERKHPWQSELLRK 425
               | |  :  ||   |||
Db         131 RLPLSQRLWQQGWLRK 146


RESULT 14
US-09-142-791A-2
; Sequence 2, Application US/09142791A
; Patent No. 6368823
; GENERAL INFORMATION:
;  APPLICANT: Antoine Michel Alain Bril
;  APPLICANT:  Thierry Paul Gerard Calmels
```

```
;  APPLICANT:  Jean-Francois Simon Pierre Faivre
;  APPLICANT:  Jean-Luc Javre
;  APPLICANT:  Sabine Rouanet
;  TITLE OF INVENTION: NOVEL COMPOUNDS
;  FILE REFERENCE: GH-30012
;  CURRENT APPLICATION NUMBER: US/09/142,791A
;  CURRENT FILING DATE:  1999-02-02
;  PRIOR APPLICATION NUMBER: PCT/EP98/01901
;  PRIOR FILING DATE: 1998-03-23
;  PRIOR APPLICATION NUMBER: UK 9706377.0
;  PRIOR FILING DATE: 1997-03-27
;  PRIOR APPLICATION NUMBER: EP 97402971.2
;  PRIOR FILING DATE: 1997-12-09
;  PRIOR APPLICATION NUMBER: EP 97403007.4
;  PRIOR FILING DATE: 1997-12-11
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 636
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-09-142-791A-2

  Query Match             4.0%;  Score 92;  DB 4;  Length 636;
  Best Local Similarity   24.1%;  Pred. No. 1.3;
  Matches   32;  Conservative   26;  Mismatches   43;  Indels   32;  Gaps    5;

Qy         25 EVVELNVGGQVYFTRHSTLISIPHSLLW---KMFSPKRDTANDLAKDSKGRFFIDRDGFL 81
              |:: ||| |: : |  :||   | :||    | |    ||           :| |||  :
Db         40 ELIVLNVSGRRFQTWRTTLERYPDTLLGSTEKEFFFNEDTK---------EYFFDRDPEV 90

Qy         82 FRYILDYLRDRQVVLPDHFPEKGRLK----REAEYFQLPDLVKLLTPDEIKQSPDEFCHS 137
              || :|:: |  ::    |:|    :       | |  ||:::             : |:
Db         91 FRCVLNFYRTGKL----HYPRYECISAYDDELAFYGILPEII-----------GDCCYE 134

Qy        138 DFEDASQGSDTRI 150
              :::|  : :  |:
Db        135 EYKDRKRENAERL 147


RESULT 15
US-09-178-109-4
; Sequence 4, Application US/09178109
; Patent No. 6395477
; GENERAL INFORMATION:
;  APPLICANT: Cockett, Mark I.
;  APPLICANT: Dilks, Daniel W.
;  APPLICANT: Chang Ling, Huai-Ping
;  APPLICANT: Sokol, Patricia T.
;  TITLE OF INVENTION: Human Potassium Channel Polynucleotides and
;  TITLE OF INVENTION: Polypeptides and Uses Therefor
;  FILE REFERENCE: ahp-98089
;  CURRENT APPLICATION NUMBER: US/09/178,109
;  CURRENT FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
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; LENGTH: 636
; TYPE: PRT
; ORGANISM: human
US-09-178-109-4

  Query Match 4.0%; Score 92; DB 4; Length 636;
  Best Local Similarity 24.1%; Pred. No. 1.3;
  Matches 32; Conservative 26; Mismatches 43; Indels 32; Gaps 5;

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Qy         25 EVVELNVGGQVYFTRHSTLISIPHSLLW---KMFSPKRDTANDLAKDSKGRFFIDRDGFL 81
              |:: ||| |: : |  :||   | :||    | |    ||          :| |||  :
Db         40 ELIVLNVSGRRFQTWRTTLERYPDTLLGSTEKEFFFNEDTK---------EYFFDRDPEV 90

Qy         82 FRYILDYLRDRQVVLPDHFPEKGRLK----REAEYFQLPDLVKLLTPDEIKQSPDEFCHS 137
              || :|:: |  ::    |:|    :       | |  ||:::             : |:
Db         91 FRCVLNFYRTGKL----HYPRYECISAYDDELAFYGILPEII-----------GDCCYE 134

Qy        138 DFEDASQGSDTRI 150
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Db        135 EYKDRKRENAERL 147
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Search completed: January 29, 2004, 02:56:18
Job time : 25 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 29, 2004, 02:52:31 ; Search time 306 Seconds
(without alignments)
289.161 Million cell updates/sec

Title: US-10-056-884A-2
Perfect score: 2284
Sequence: 1 MALSGNCSRYYPREQGSAVP.....DRFPERKHPWQSELLRKYHL 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	2284	100.0	428	15	US-10-056-884-2	Sequence 2, Appli
2	2271	99.4	435	15	US-10-080-980-4	Sequence 4, Appli
3	832	36.4	325	15	US-10-080-980-2	Sequence 2, Appli
4	541	23.7	103	15	US-10-056-884-20	Sequence 20, Appl
5	538.5	23.6	228	15	US-10-056-884-5	Sequence 5, Appli
6	538.5	23.6	228	15	US-10-080-980-3	Sequence 3, Appli
7	367	16.1	101	15	US-10-080-980-13	Sequence 13, Appl
8	345.5	15.1	190	15	US-10-056-884-6	Sequence 6, Appli
9	234.5	10.3	351	15	US-10-086-156-2	Sequence 2, Appli
10	226	9.9	99	15	US-10-086-156-12	Sequence 12, Appl
11	210	9.2	256	12	US-10-234-951A-4	Sequence 4, Appli
12	210	9.2	256	15	US-10-056-884-7	Sequence 7, Appli
13	210	9.2	256	15	US-10-080-980-6	Sequence 6, Appli
14	210	9.2	256	15	US-10-121-746-14	Sequence 14, Appl
15	210	9.2	256	15	US-10-086-156-4	Sequence 4, Appli
16	210	9.2	257	12	US-10-234-951A-6	Sequence 6, Appli
17	210	9.2	257	15	US-10-192-116A-6	Sequence 6, Appli
18	210	9.2	257	15	US-10-071-458-3	Sequence 3, Appli
19	204	8.9	213	12	US-10-168-651-11	Sequence 11, Appl
20	204	8.9	213	14	US-10-024-579-2	Sequence 2, Appli
21	203	8.9	528	15	US-10-192-116A-2	Sequence 2, Appli
22	202.5	8.9	237	12	US-10-234-951A-3	Sequence 3, Appli
23	202.5	8.9	237	12	US-10-264-171-3	Sequence 3, Appli
24	202.5	8.9	237	15	US-10-040-805-3	Sequence 3, Appli
25	202.5	8.9	237	15	US-10-056-884-4	Sequence 4, Appli
26	202.5	8.9	237	15	US-10-080-980-7	Sequence 7, Appli
27	202.5	8.9	237	15	US-10-080-980-9	Sequence 9, Appli
28	202.5	8.9	237	15	US-10-121-746-25	Sequence 25, Appl
29	202.5	8.9	237	15	US-10-086-156-3	Sequence 3, Appli
30	202.5	8.9	237	15	US-10-071-458-6	Sequence 6, Appli
31	201.5	8.8	257	14	US-10-024-579-14	Sequence 14, Appl
32	201.5	8.8	283	14	US-10-024-579-10	Sequence 10, Appl
33	193.5	8.5	140	15	US-10-080-980-5	Sequence 5, Appli
34	191	8.4	75	12	US-09-864-408A-7362	Sequence 7362, Ap
35	189	8.3	225	15	US-10-086-156-25	Sequence 25, Appl
36	189	8.3	255	12	US-10-168-651-4	Sequence 4, Appli
37	189	8.3	255	12	US-10-264-171-2	Sequence 2, Appli
38	189	8.3	255	15	US-10-040-805-2	Sequence 2, Appli
39	189	8.3	258	12	US-10-234-951A-5	Sequence 5, Appli
40	189	8.3	258	15	US-10-121-746-12	Sequence 12, Appl
41	185	8.1	197	15	US-10-106-698-4675	Sequence 4675, Ap
42	184	8.1	175	9	US-09-925-299-879	Sequence 879, App
43	184	8.1	175	11	US-09-925-299-879	Sequence 879, App
44	174.5	7.6	238	14	US-10-024-579-16	Sequence 16, Appl
45	174.5	7.6	264	14	US-10-024-579-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-10-056-884-2
; Sequence 2, Application US/10056884
; Publication No. US20030032786A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company

```
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNIT,
;  TITLE OF INVENTION:  K+betaM2
;  FILE REFERENCE: D0076 NP
;  CURRENT APPLICATION NUMBER: US/10/056,884
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: US 60/263,872
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: US 60/269,794
;  PRIOR FILING DATE: 2001-02-14
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 428
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-056-884-2

  Query Match             100.0%;  Score 2284;  DB 15;  Length 428;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-215;
  Matches  428;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 60
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Db          1 MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 60

Qy         61 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVK 120

Qy        121 LLTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LLTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREG 180

Qy        181 QADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFKHLERAFDML 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 QADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFKHLERAFDML 240

Qy        241 SECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 SECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 300

Qy        301 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEMR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEMR 360

Qy        361 RKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 RKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS 420

Qy        421 ELLRKYHL 428
              ||||||||
Db        421 ELLRKYHL 428


RESULT 2
US-10-080-980-4
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; Sequence 4, Application US/10080980
; Publication No. US20030036115A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT,
; TITLE OF INVENTION: K+betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE
; FILE REFERENCE: D0121 NP
; CURRENT APPLICATION NUMBER: US/10/080,980
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,132
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/278,953
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 435
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-080-980-4

  Query Match   99.4%; Score 2271; DB 15; Length 435;
  Best Local Similarity   99.5%; Pred. No. 1.3e-213;
  Matches 426; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

```
Qy          1 MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 67

Qy         61 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVK 127

Qy        121 LLTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 LLTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREG 187

Qy        181 QADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFKHLERAFDML 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 QADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFKHLERAFDML 247

Qy        241 SECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 SECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 307

Qy        301 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEMR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEMR 367

Qy        361 RKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS 420
              ||||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        368 RKSDLLRTLTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKIKIPDRFPERKHPWQS 427

Qy        421 ELLRKYHL 428
              ||||||||
Db        428 ELLRKYHL 435
```

RESULT 3
US-10-080-980-2
; Sequence 2, Application US/10080980
; Publication No. US20030036115A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT,
; TITLE OF INVENTION: K+betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE
; FILE REFERENCE: D0121 NP
; CURRENT APPLICATION NUMBER: US/10/080,980
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,132
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/278,953
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 325
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-080-980-2

Query Match 36.4%; Score 832; DB 15; Length 325;
Best Local Similarity 54.0%; Pred. No. 8.6e-73;
Matches 170; Conservative 41; Mismatches 56; Indels 48; Gaps 6;

```
Qy          4 SGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTAN 63
              ||: |        || |  ||::||||||||||| ||  |::|:| ||||:||: ::
Db         20 SGSSS-------SSAEPPLFPDIVELNVGGQVYVTRRCTVVSVPDSLLWRMFTQQQ--PQ 70

Qy         64 DLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLL- 122
              :||:|||||||:|||||||||||||||| |:||||:|||: ||:|||||:||:||: |
Db         71 ELARDSKGRFFLDRDGFLFRYILDYLRDLQLVLPDYFPERSRLQREAEYFELPELVRRLG 130

Qy        123 TPDEIKQSP--------------DEFCHSDFEDASQ----------------------GS 146
               | :    |              ||     : :  |                      |:
Db        131 APQQPGPGPPPSRRGVHKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGA 190

Qy        147 DTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVFG 206
                 :  ||  |   |: |:||:||||| |:||: ||||||||| || |||: ||||||||
Db        191 AGPLLTPSQSLDGSRRSGYITIGYRGSYTIGRDAQADAKFRRVARITVCGKTSLAKEVFG 250

Qy        207 ETLNESRDPDRAPERYTSRFYLKFKHLERAFDMLSECGFHMVACNSSVTASFIN--QYTD 264
              :|||||||||| |||||||:||||  ||:||| ||| |||||||:|: | :| :    ::
Db        251 DTLNESRDPDRPPERYTSRYYLKFNFLEQAFDKLSESGFHMVACSSTGTCAFASSTDQSE 310

Qy        265 DKIWSSYTEYVFYRE 279
              ||||:||||||| ||
Db        311 DKIWTSYTEYVFCRE 325
```

RESULT 4
US-10-056-884-20

; Sequence 20, Application US/10056884
; Publication No. US20030032786A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT,
; TITLE OF INVENTION: K+betaM2
; FILE REFERENCE: D0076 NP
; CURRENT APPLICATION NUMBER: US/10/056,884
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,872
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/269,794
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-056-884-20

Query Match 23.7%; Score 541; DB 15; Length 103;
Best Local Similarity 100.0%; Pred. No. 5.1e-45;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRY 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRY 60

Qy          85 ILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEI 127
               |||||||||||||||||||||||||||||||||||||||||||
Db          61 ILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEI 103
```

RESULT 5
US-10-056-884-5
; Sequence 5, Application US/10056884
; Publication No. US20030032786A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT,
; TITLE OF INVENTION: K+betaM2
; FILE REFERENCE: D0076 NP
; CURRENT APPLICATION NUMBER: US/10/056,884
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,872
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/269,794
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Drosophila melanogaster

US-10-056-884-5

```
  Query Match             23.6%;  Score 538.5;  DB 15;  Length 228;
  Best Local Similarity   44.3%;  Pred. No. 2.9e-44;
  Matches  116;  Conservative   44;  Mismatches   61;  Indels   41;  Gaps    7;

Qy         24 PEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFR 83
              ||::|||||| | |  :||:    :|| ::|   ||:   ||||||||:|:|||| |||
Db          2 PEIIELNVGGVSYTTTLATLLQDKSTLLAELFGEGRDS---LAKDSKGRYFLDRDGVLFR 58

Qy         84 YILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDAS 143
              ||||:|||: : ||: | |: || ||||:|:|  ::: :  :
Db         59 YILDFLRDKALHLPEGFRERQRLLREAEHFKLTAMLECIRSER---------------- 101

Qy        144 QGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKE 203
                | |  ||          | ||:|||||   |::| || |||:: |||||||::  :|
Db        102 ---DAR--PP----------GCITIGYRGSFQFGKDGLADVKFRKLSRILVCGRVAQCRE 146

Qy        204 VFGETLNESRDPDR-APERYTSRFYLKFKHLERAFDMLSECGFHMV-ACNSSVTASFINQ 261
              |||:|||||||||    :||||||:||  ::|:||| | : |: |  :| |    |
Db        147 VFGDTLNESRDPDHGGTDRYTSRFFLKHCYIEQAFDNLHDHGYRMAGSCGSGTAGSAAEP 206

Qy        262 Y----TDDKIWSSYTEYVFYRE 279
                   |::  |: | |:|| |:
Db        207 KPGVDTEENRWNHYNEFVFIRD 228
```

RESULT 6
US-10-080-980-3
; Sequence 3, Application US/10080980
; Publication No. US20030036115A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT,
; TITLE OF INVENTION: K+betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE
; FILE REFERENCE: D0121 NP
; CURRENT APPLICATION NUMBER: US/10/080,980
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,132
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/278,953
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 228
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-10-080-980-3

```
  Query Match             23.6%;  Score 538.5;  DB 15;  Length 228;
  Best Local Similarity   44.3%;  Pred. No. 2.9e-44;
  Matches  116;  Conservative   44;  Mismatches   61;  Indels   41;  Gaps    7;

Qy         24 PEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFR 83
              ||::|||||| | |  :||:    :|| ::|   ||:   ||||||||:|:|||| |||
```

```
Db          2 PEIIELNVGGVSYTTTLATLLQDKSTLLAELFGEGRDS---LAKDSKGRYFLDRDGVLFR 58

Qy         84 YILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDAS 143
              ||||:|||: : ||: | |: || ||||:|:|  ::: :  :
Db         59 YILDFLRDKALHLPEGFRERQRLLREAEHFKLTAMLECIRSER---------------- 101

Qy        144 QGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKE 203
                 | |  ||          | ||:|||||   |::| || |||:: |||||||::  :|
Db        102 ---DAR--PP----------GCITIGYRGSFQFGKDGLADVKFRKLSRILVCGRVAQCRE 146

Qy        204 VFGETLNESRDPDR-APERYTSRFYLKFKHLERAFDMLSECGFHMV-ACNSSVTASFINQ 261
              |||:|||||||||    :||||||:||  ::|:||| | : |: |  :| |    |
Db        147 VFGDTLNESRDPDHGGTDRYTSRFFLKHCYIEQAFDNLHDHGYRMAGSCGSGTAGSAAEP 206

Qy        262 Y----TDDKIWSSYTEYVFYRE 279
                   |::  |: | |:|| |:
Db        207 KPGVDTEENRWNHYNEFVFIRD 228


RESULT 7
US-10-080-980-13
; Sequence 13, Application US/10080980
; Publication No. US20030036115A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNIT,
;  TITLE OF INVENTION:  K+betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE
;  FILE REFERENCE: D0121 NP
;  CURRENT APPLICATION NUMBER: US/10/080,980
;  CURRENT FILING DATE:  2002-02-21
;  PRIOR APPLICATION NUMBER: US 60/270,132
;  PRIOR FILING DATE: 2001-02-21
;  PRIOR APPLICATION NUMBER: US 60/278,953
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
;   LENGTH: 101
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-080-980-13

  Query Match             16.1%;  Score 367;  DB 15;  Length 101;
  Best Local Similarity   68.4%;  Pred. No. 5.6e-28;
  Matches   67;  Conservative   19;  Mismatches   10;  Indels    2;  Gaps    1;

Qy         25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRY 84
              ::||||||||||| ||  |::|:| ||||:||: ::    :||:|||||||:|||||||||
Db          1 DIVELNVGGQVYVTRRCTVVSVPDSLLWRMFTQQQ--PQELARDSKGRFFLDRDGFLFRY 58

Qy         85 ILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLL 122
              ||||||| |:||||:|||: ||:||||||:||:||: |
Db         59 ILDYLRDLQLVLPDYFPERSRLQREAEYFELPELVRRL 96


RESULT 8
```

US-10-056-884-6
; Sequence 6, Application US/10056884
; Publication No. US20030032786A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNIT,
; TITLE OF INVENTION: K+betaM2
; FILE REFERENCE: D0076 NP
; CURRENT APPLICATION NUMBER: US/10/056,884
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/263,872
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: US 60/269,794
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-056-884-6

Query Match 15.1%; Score 345.5; DB 15; Length 190;
Best Local Similarity 39.6%; Pred. No. 1.8e-25;
Matches 80; Conservative 34; Mismatches 59; Indels 29; Gaps 4;

```
Qy          22 SFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSK--------GRF 73
               |  :|: ||||| :| |  |||     :||  : |        |::| :         |
Db           3 SVEDVITLNVGGTMYTTTRSTLSKETDTLLANIAS------GSLSEDEQANVVTLPDGTL 56

Qy          74 FIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDE 133
               |:|||| || |:| :||  :: ||: | |  ||| ||:::::|     ||: :    ||
Db          57 FVDRDGPLFAYVLHFLRTDKLSLPEQFREVARLKDEADFYRLERFSTLLS-NASSISPRP 115

Qy         134 FCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRIL 193
                  : :   : |::|               |:||:||||:   ||:|||| |||:: |||
Db         116 RTANGYNTITSGAET--------------GGYITLGYRGTFAFGRDGQADVKFRKLHRIL 161

Qy         194 VCGRISLAKEVFGETLNESRDP 215
               |||| :| :||| :||||||||
Db         162 VCGRATLCREVFADTLNESRDP 183
```

RESULT 9
US-10-086-156-2
; Sequence 2, Application US/10086156
; Publication No. US20030054989A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNITS,
; TITLE OF INVENTION: K+betaM4 and K+betaM5
; FILE REFERENCE: D0115NP
; CURRENT APPLICATION NUMBER: US/10/086,156
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/272,190

```
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: US 60/274,258
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 98
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
;   LENGTH: 351
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-086-156-2

  Query Match             10.3%;  Score 234.5;  DB 15;  Length 351;
  Best Local Similarity   40.3%;  Pred. No. 3.4e-14;
  Matches   52;  Conservative   26;  Mismatches   44;  Indels    7;  Gaps    2;

Qy          8 SRYYPREQGSAVPNSFP---EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTAND 64
              :|::   :|       |   : : |||||::| |  :|| | | |:|  ||| |  |
Db         74 TRFFSCREGLLPATQSPAMSDPITLNVGGKLYTTSLATLTSFPDSMLGAMFSGKMPT--- 130

Qy         65 LAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTP 124
               :||:|  |||||| :||||||::||   : ||: | | | |:|||:::|:  |:: |
Db        131 -KRDSQGNCFIDRDGKVFRYILNFLRTSHLDLPEDFQEMGLLRREADFYQVQPLIEALQE 189

Qy        125 DEIKQSPDE 133
              |:: |  |
Db        190 KEVELSKAE 198


RESULT 10
US-10-086-156-12
; Sequence 12, Application US/10086156
; Publication No. US20030054989A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNITS,
;  TITLE OF INVENTION:  K+betaM4 and K+betaM5
;  FILE REFERENCE: D0115NP
;  CURRENT APPLICATION NUMBER: US/10/086,156
;  CURRENT FILING DATE:  2002-02-28
;  PRIOR APPLICATION NUMBER: US 60/272,190
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: US 60/274,258
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 98
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
;   LENGTH: 99
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-10-086-156-12

  Query Match              9.9%;  Score 226;  DB 15;  Length 99;
  Best Local Similarity   46.5%;  Pred. No. 3.6e-14;
  Matches   47;  Conservative   20;  Mismatches   30;  Indels    4;  Gaps    1;

Qy         27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYIL 86
```

```
              : ||||||::| |  :|| | | |:|  ||| |  |     :||:|  |||||| :|||||
Db             3 ITLNVGGKLYTTSLATLTSFPDSMLGAMFSGKMPT----KRDSQGNCFIDRDGKVFRYIL 58

Qy            87 DYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEI 127
                 ::||   : ||: | | | |:|||:::|:  |:: |   |:
Db            59 NFLRTSHLDLPEDFQEMGLLRREADFYQVQPLIEALQEKEV 99


RESULT 11
US-10-234-951A-4
; Sequence 4, Application US/10234951A
; Publication No. US20030162251A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
;  TITLE OF INVENTION:  BETA-SUBUNIT, K+betaM8
;  FILE REFERENCE: D0162 NP
;  CURRENT APPLICATION NUMBER: US/10/234,951A
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: U.S. 60/317,087
;  PRIOR FILING DATE: 2001-09-04
;  PRIOR APPLICATION NUMBER: U.S. 60/329,666
;  PRIOR FILING DATE: 2001-10-16
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: wherein "X" equals any amino acid.
US-10-234-951A-4

  Query Match             9.2%;  Score 210;  DB 12;  Length 256;
  Best Local Similarity   28.7%;  Pred. No. 5.4e-12;
  Matches   77;  Conservative   39;  Mismatches   82;  Indels   70;  Gaps   12;

Qy            27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDS-KGRFFIDRDGFLFRYI 85
                 | ::||| :| :  :||   | | : ::|    |    :  || |  :|||||| :||||
Db            32 VHIDVGGHMYTSSLATLTKYPESRIGRLF----DGTEPIVLDSLKQHYFIDRDGQMFRYI 87

Qy            86 LDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQG 145
                 |::||  ::::|| | :   |  ||:||||  :  ||  :  ||           |   |
Db            88 LNFLRTSKLLIPDDFKDYTLLYEEAKYFQLQPM--LLEMERWKQ----------DRETG 134

Qy           146 SDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVF 205
                   :| |                :  | :  ||             || : |  || :|||
Db           135 RFSRPCE-------------CLVVRVAPDLGE-----------RITLSGDKSLIEEVF 168

Qy           206 GE-------TLNESRDPDRAPERYTSRFYLK-FKHLE--RAFDMLSECGFHMV-ACNSSV 254
                 |       ::|   : |     :  || |  : ||   :  : | : || :| :|   |
Db           169 PEIGDVMCNSVNAGWNHD---STHVIRFPLNGYCHLNSVQVLERLQQRGFEIVGSCGGGV 225

Qy           255 TASFINQYTDDKIWSSYTEYVFYREPSR 282
                  :            | ::|||  ||  |
```

```
Db        226 DS------------SQFSEYVLRRELRR 241


RESULT 12
US-10-056-884-7
; Sequence 7, Application US/10056884
; Publication No. US20030032786A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNIT,
;  TITLE OF INVENTION:  K+betaM2
;  FILE REFERENCE: D0076 NP
;  CURRENT APPLICATION NUMBER: US/10/056,884
;  CURRENT FILING DATE:  2002-01-24
;  PRIOR APPLICATION NUMBER: US 60/263,872
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: US 60/269,794
;  PRIOR FILING DATE: 2001-02-14
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: variant
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: wherein "Xaa" is unknown.
US-10-056-884-7

  Query Match             9.2%;  Score 210;  DB 15;  Length 256;
  Best Local Similarity   28.7%;  Pred. No. 5.4e-12;
  Matches   77;  Conservative   39;  Mismatches   82;  Indels   70;  Gaps   12;

Qy         27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDS-KGRFFIDRDGFLFRYI 85
              | ::||| :| :  :||   | | : ::|    |    :  || |  :|||||| :||||
Db         32 VHIDVGGHMYTSSLATLTKYPESRIGRLF----DGTEPIVLDSLKQHYFIDRDGQMFRYI 87

Qy         86 LDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQG 145
              |::||  ::::|| | :   |  ||:||||  :  ||  :  ||           |   |
Db         88 LNFLRTSKLLIPDDFKDYTLLYEEAKYFQLQPM--LLEMERWKQ-----------DRETG 134

Qy        146 SDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVF 205
               :| |                :  | :  ||             || : |  || :|||
Db        135 RFSRPCE--------------CLVVRVAPDLGE-----------RITLSGDKSLIEEVF 168

Qy        206 GE-------TLNESRDPDRAPERYTSRFYLK-FKHLE--RAFDMLSECGFHMV-ACNSSV 254
               |       ::|   : |     :  || |  : ||   :  : | : || :| :|   |
Db        169 PEIGDVMCNSVNAGWNHD---STHVIRFPLNGYCHLNSVQVLERLQQRGFEIVGSCGGGV 225

Qy        255 TASFINQYTDDKIWSSYTEYVFYREPSR 282
               :           | ::|||  ||  |
Db        226 DS------------SQFSEYVLRRELRR 241


RESULT 13
```

US-10-080-980-6
; Sequence 6, Application US/10080980
; Publication No. US20030036115A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN POTASSIUM CHANNEL
BETA-SUBUNIT,
; TITLE OF INVENTION: K+betaM6, EXPRESSED HIGHLY IN THE SMALL INTESTINE
; FILE REFERENCE: D0121 NP
; CURRENT APPLICATION NUMBER: US/10/080,980
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 60/270,132
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/278,953
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: wherein "X" is equal to any amino acid.
US-10-080-980-6

  Query Match   9.2%; Score 210; DB 15; Length 256;
  Best Local Similarity   28.7%; Pred. No. 5.4e-12;
  Matches   77; Conservative   39; Mismatches   82; Indels   70; Gaps   12;

```
Qy          27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDS-KGRFFIDRDGFLFRYI 85
               | ::||| :| :  :||   | | : ::|    |    :  || |  :|||||| :|||| 
Db          32 VHIDVGGHMYTSSLATLTKYPESRIGRLF----DGTEPIVLDSLKQHYFIDRDGQMFRYI 87

Qy          86 LDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQG 145
               |::||  ::::|| | :   |  ||:||||  :  ||  :  ||           |   |
Db          88 LNFLRTSKLLIPDDFKDYTLLYEEAKYFQLQPM--LLEMERWKQ----------DRETG 134

Qy         146 SDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVF 205
                :| |                :  | :  ||              || : |  || :|||
Db         135 RFSRPCE--------------CLVVRVAPDLGE-----------RITLSGDKSLIEEVF 168

Qy         206 GE-------TLNESRDPDRAPERYTSRFYLK-FKHLE--RAFDMLSECGFHMV-ACNSSV 254
                |       ::|   : |     :  || |  : ||   :  : | : || :| :|   |
Db         169 PEIGDVMCNSVNAGWNHD---STHVIRFPLNGYCHLNSVQVLERLQQRGFEIVGSCGGGV 225

Qy         255 TASFINQYTDDKIWSSYTEYVFYREPSR 282
                :            | ::|||  ||  |
Db         226 DS------------SQFSEYVLRRELRR 241
```

RESULT 14
US-10-121-746-14
; Sequence 14, Application US/10121746
; Publication No. US20030036648A1
; GENERAL INFORMATION:

```
;  APPLICANT: Miller, Andrew P.
;  APPLICANT:  Curran, Mark Edward
;  APPLICANT:  Hu, Ping
;  APPLICANT:  Rutter, Marc
;  APPLICANT:  Wang, Jian-Wang
;  TITLE OF INVENTION: No. US20030036648A1el Human Potassium Channels
;  FILE REFERENCE: SEQ-15P
;  CURRENT APPLICATION NUMBER: US/10/121,746
;  CURRENT FILING DATE:  2002-04-11
;  PRIOR APPLICATION NUMBER: US/09/336,643A
;  PRIOR FILING DATE: 1999-06-18
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: H. sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (1)...(256)
;   OTHER INFORMATION: Xaa = Any Amino Acid
US-10-121-746-14

  Query Match             9.2%;  Score 210;  DB 15;  Length 256;
  Best Local Similarity   28.7%;  Pred. No. 5.4e-12;
  Matches   77;  Conservative   39;  Mismatches   82;  Indels   70;  Gaps   12;

Qy         27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDS-KGRFFIDRDGFLFRYI 85
              | ::||| :| :  :||   | | : ::|    |    :  || |  :|||||| :||||
Db         32 VHIDVGGHMYTSSLATLTKYPESRIGRLF----DGTEPIVLDSLKQHYFIDRDGQMFRYI 87

Qy         86 LDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQG 145
              |::||  ::::|| | :   |  ||:||||  :  ||  :  ||           |   |
Db         88 LNFLRTSKLLIPDDFKDYTLLYEEAKYFQLQPM--LLEMERWKQ----------DRETG 134

Qy        146 SDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVF 205
               :| |                :  | :  ||             || : |  || :|||
Db        135 RFSRPCE--------------CLVVRVAPDLGE-----------RITLSGDKSLIEEVF 168

Qy        206 GE-------TLNESRDPDRAPERYTSRFYLK-FKHLE--RAFDMLSECGFHMV-ACNSSV 254
               |       ::|   : |     :  || |  : ||   :  : | : || :| :|   |
Db        169 PEIGDVMCNSVNAGWNHD---STHVIRFPLNGYCHLNSVQVLERLQQRGFEIVGSCGGGV 225

Qy        255 TASFINQYTDDKIWSSYTEYVFYREPSR 282
               :            | ::|||  ||  |
Db        226 DS------------SQFSEYVLRRELRR 241


RESULT 15
US-10-086-156-4
; Sequence 4, Application US/10086156
```

; Publication No. US20030054989A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING TWO NOVEL HUMAN POTASSIUM CHANNEL BETA-SUBUNITS,
; TITLE OF INVENTION: K+betaM4 and K+betaM5
; FILE REFERENCE: D0115NP
; CURRENT APPLICATION NUMBER: US/10/086,156
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/272,190
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/274,258
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: homo sapiens
;   FEATURE:
;   NAME/KEY: UNSURE
;   LOCATION: (15)..(15)
;   OTHER INFORMATION: wherein "X" is equal to any amino acid.
US-10-086-156-4

  Query Match   9.2%; Score 210; DB 15; Length 256;
  Best Local Similarity   28.7%; Pred. No. 5.4e-12;
  Matches   77; Conservative   39; Mismatches   82; Indels   70; Gaps   12;

```
Qy         27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDS-KGRFFIDRDGFLFRYI 85
              | ::||| :| :  :||   | | : ::|    |    :  || |  :|||||| :||||
Db         32 VHIDVGGHMYTSSLATLTKYPESRIGRLF----DGTEPIVLDSLKQHYFIDRDGQMFRYI 87

Qy         86 LDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQG 145
              |::||  ::::|| | :   |  ||:||||  :  ||  :  ||           |   |
Db         88 LNFLRTSKLLIPDDFKDYTLLYEEAKYFQLQPM--LLEMERWKQ-----------DRETG 134

Qy        146 SDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVF 205
               :| |                :  | :  ||             || : |  || :|||
Db        135 RFSRPCE--------------CLVVRVAPDLGE-----------RITLSGDKSLIEEVF 168

Qy        206 GE-------TLNESRDPDRAPERYTSRFYLK-FKHLE--RAFDMLSECGFHMV-ACNSSV 254
               |       ::|   : |     :  || |  : ||   :  : | : || :| :|   |
Db        169 PEIGDVMCNSVNAGWNHD---STHVIRFPLNGYCHLNSVQVLERLQQRGFEIVGSCGGGV 225

Qy        255 TASFINQYTDDKIWSSYTEYVFYREPSR 282
               :            | ::|||  ||  |
Db        226 DS------------SQFSEYVLRRELRR 241
```

Search completed: January 29, 2004, 03:01:31
Job time : 307 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 29, 2004, 02:33:16 ; Search time 28 Seconds
(without alignments)
1470.007 Million cell updates/sec

Title: US-10-056-884A-2
Perfect score: 2284
Sequence: 1 MALSGNCSRYYPREQGSAVP.....DRFPERKHPWQSELLRKYHL 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	345.5	15.1	190	2	T26019	hypothetical prote
2	169.5	7.4	207	2	T31996	hypothetical prote
3	158.5	6.9	272	2	T15820	hypothetical prote
4	158	6.9	670	2	T32221	hypothetical prote
5	156	6.8	220	2	T20366	hypothetical prote
6	146.5	6.4	220	2	T33592	hypothetical prote
7	146	6.4	348	2	A41784	tumor necrosis fac
8	145.5	6.4	179	2	T33590	hypothetical prote
9	144	6.3	212	2	T31997	hypothetical prote
10	131.5	5.8	373	2	T26685	hypothetical prote
11	122.5	5.4	231	2	T32070	hypothetical prote
12	122.5	5.4	236	2	T33589	hypothetical prote
13	121.5	5.3	246	2	T25978	hypothetical prote

14	119	5.2	277	2	T21630	hypothetical prote
15	115.5	5.1	134	2	T32065	hypothetical prote
16	115	5.0	204	2	T25972	hypothetical prote
17	115	5.0	244	2	T25970	hypothetical prote
18	115	5.0	347	2	T31922	hypothetical prote
19	114.5	5.0	208	2	T25973	hypothetical prote
20	114	5.0	155	2	T25980	hypothetical prote
21	113.5	5.0	140	2	T25976	hypothetical prote
22	111	4.9	155	2	T25979	hypothetical prote
23	105	4.6	139	2	T32068	hypothetical prote
24	105	4.6	441	2	C84634	hypothetical prote
25	105	4.6	1504	2	A33602	DNA-directed DNA p
26	104.5	4.6	1176	2	A49848	nitrite reductase
27	104	4.6	108	2	T22320	hypothetical prote
28	104	4.6	294	2	T33588	hypothetical prote
29	104	4.6	490	2	A35312	potassium channel
30	104	4.6	491	2	JE0276	voltage-gated pota
31	103.5	4.5	84	2	T25977	hypothetical prote
32	103.5	4.5	140	2	A88479	protein F47D12.3 [
33	103	4.5	139	2	T25974	hypothetical prote
34	102	4.5	326	2	T32067	hypothetical prote
35	101.5	4.4	1537	2	JC4172	DNA (cytosine-5-)-
36	100.5	4.4	651	2	A39372	potassium channel
37	100	4.4	265	2	T32015	hypothetical prote
38	100	4.4	737	2	S18207	adducin alpha chai
39	99	4.3	232	2	D88076	protein K02F6.8 [i
40	98.5	4.3	745	2	T39952	hypothetical prote
41	98	4.3	329	2	A31595	interferon regulat
42	98	4.3	825	2	S26706	transcription fact
43	97.5	4.3	1213	2	A41724	limb deformity (ld
44	97	4.2	441	2	C85362	hypothetical prote
45	96.5	4.2	784	2	D96564	myosin-like protei

ALIGNMENTS

RESULT 1
T26019
hypothetical protein VM106R.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26019
R;Barlow, K.
submitted to the EMBL Data Library, August 1998
A;Reference number: Z20135
A;Accession: T26019
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-190 <WIL>
A;Cross-references: EMBL:AL031266; PIDN:CAA20329.1; GSPDB:GN00020; CESP:VM106R.1
A;Experimental source: clone VM106R
C;Genetics:
A;Gene: CESP:VM106R.1
A;Map position: 2
A;Introns: 131/1

```
  Query Match             15.1%;  Score 345.5;  DB 2;  Length 190;
  Best Local Similarity   39.6%;  Pred. No. 8.5e-21;
  Matches   80;  Conservative   34;  Mismatches   59;  Indels   29;  Gaps    4;

Qy         22 SFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSK--------GRF 73
              |  :|: ||||| :| |  |||     :||  : |        |::| :        |
Db          3 SVEDVITLNVGGTMYTTTRSTLSKETDTLLANIAS------GSLSEDEQANVVTLPDGTL 56

Qy         74 FIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDE 133
              |:|||| || |:| :||  :: ||: | |  ||| ||:::|     ||: :    ||
Db         57 FVDRDGPLFAYVLHFLRTDKLSLPEQFREVARLKDEADFYRLERFSTLLS-NASSISPRP 115

Qy        134 FCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRIL 193
                 : :   : |::|               |:||:||||:   ||:|||| |||:: |||
Db        116 RTANGYNTITSGAET--------------GGYITLGYRGTFAFGRDGQADVKFRKLHRIL 161

Qy        194 VCGRISLAKEVFGETLNESRDP 215
              |||| :| :||| :||||||||
Db        162 VCGRATLCREVFADTLNESRDP 183


RESULT 2
T31996
hypothetical protein B0281.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
C;Accession: T31996
R;Pauley, A.; Scheet, P.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid B0281.
A;Reference number: Z21109
A;Accession: T31996
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-207 <PAU>
A;Cross-references: EMBL:AF016666; PIDN:AAB66084.1; GSPDB:GN00020; CESP:B0281.5
A;Experimental source: strain Bristol N2; clone B0281
C;Genetics:
A;Gene: CESP:B0281.5
A;Map position: 2
A;Introns: 38/3; 120/3; 160/1
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC239.12

  Query Match              7.4%;  Score 169.5;  DB 2;  Length 207;
  Best Local Similarity   27.6%;  Pred. No. 2.2e-06;
  Matches   69;  Conservative   21;  Mismatches   83;  Indels   77;  Gaps   10;

Qy         27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYIL 86
              |:|||||  |: |  |||    |   :|      :|     ||    |||||    |  :|
Db          6 VKLNVGGTVFETLKSTLTK--HDGFFKALI---ETDVPAEKDDSNCFFIDRSPKHFETVL 60

Qy         87 DYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQGS 146
              :|:|   |||||   :   ||:||||: | :| ||  |       | |
Db         61 NYMRSGDVVLPDSKKDMLELKKEAEYYLLSNLAKLCQP-----PTDNF------------ 103

Qy        147 DTRICPPSSLL----PADRK----------------WGFITVGYRGSCTLGREGQADAK 185
                : | |  |:      |:|                 |||  | :       |:   |
```

```
Db        104 --KTCTPEELMRVVANTDKKVIMINYLTYNGELVFYPWGFNLVHF---LIQNRDYVEDVY 158

Qy        186 FRRVPRILVCGRISLAKEVFGETLNESRDPDRAP-----ERYTSRFYLKFKHLERAFDM- 239
              |||                        ||: |:  |       :|   |   :   | |
Db        159 FRR---------------------TESQYPEDGPFPNEKPYWTFLVYNSTRSGRRPFRHT 197

Qy        240 --LSECGFHM 247
                | :|  ||
Db        198 VDLEDCMGHM 207


RESULT 3
T15820
hypothetical protein C52B11.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15820
R;Martin, J.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C52B11.
A;Reference number: Z18411
A;Accession: T15820
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-272 <MAR>
A;Cross-references: EMBL:U41276; NID:g1086884; PID:g1086886; PIDN:AAA82468.1;
CESP:C52B11.2
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:C52B11.2
A;Introns: 12/1; 91/3; 190/3; 221/3

  Query Match             6.9%;  Score 158.5;  DB 2;  Length 272;
  Best Local Similarity   32.3%;  Pred. No. 2.5e-05;
  Matches   40;  Conservative   26;  Mismatches   43;  Indels   15;  Gaps    4;

Qy         27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYIL 86
              | |||||:|: |  |||:  | | |:::   :     |  :|  | : ||||   |  ||
Db         84 VRLNVGGKVFQTTRSTLMREPCSFLYRLCQDEMGLPTD--RDETGAYLIDRDPDFFSPIL 141

Qy         87 DYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLL------TPDEIKQSPDEF------ 134
              :|||  ::::     |:| |  ||::: || | :|:        : :| : ::|
Db        142 NYLRHGKLIMNPGLSEEGIL-AEADFYNLPSLSQLIMDRIQDRENSVKDATNKFVYRVLQ 200

Qy        135 CHSD 138
              || :
Db        201 CHEE 204


RESULT 4
T32221
hypothetical protein T23B12.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32221
R;Davidson, S.; Wohldmann, P.; Gillam, B.
submitted to the EMBL Data Library, September 1997
```

A;Description: The sequence of C. elegans cosmid T23B12.
A;Reference number: Z21137
A;Accession: T32221
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-670 <DAV>
A;Cross-references: EMBL:AF022982; PIDN:AAB69932.1; GSPDB:GN00023; CESP:T23B12.6
A;Experimental source: strain Bristol N2; clone T23B12
C;Genetics:
A;Gene: CESP:T23B12.6
A;Map position: 5
A;Introns: 87/2; 185/3; 293/1; 400/1; 457/1; 540/2; 635/3

  Query Match   6.9%; Score 158; DB 2; Length 670;
  Best Local Similarity   41.8%; Pred. No. 8.8e-05;
  Matches   41; Conservative   15; Mismatches   36; Indels   6; Gaps   2;

Qy   26 VVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYI 85
              :| |||||::: | :|| || | : | : :: || | ||||| ||| |
Db   20 IVNLNVGGRIFATSCNTLTWIPDSFFTSLLSGRMNS----VKDPSGAIFIDRDPDLFRVI 75

Qy   86 LDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLT 123
              |:||| :|| | : || || :| | |:: ||
Db   76 LNYLRTKQVDLCG--IKVDTLKHEALFFGLTPLIRRLT 111

RESULT 5
T20366
hypothetical protein D2045.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20366
R;Lloyd, C.
submitted to the EMBL Data Library, August 1994
A;Reference number: Z19262
A;Accession: T20366
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-220 <WIL>
A;Cross-references: EMBL:Z35639; PIDN:CAA84696.1; GSPDB:GN00021; CESP:D2045.8
A;Experimental source: clone D2045
C;Genetics:
A;Gene: CESP:D2045.8
A;Map position: 3
A;Introns: 39/3; 127/3; 169/1; 194/3

  Query Match   6.8%; Score 156; DB 2; Length 220;
  Best Local Similarity   37.8%; Pred. No. 3e-05;
  Matches   42; Conservative   21; Mismatches   42; Indels   6; Gaps   3;

Qy   26 VVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYI 85
              :|:|:|||::: | || |:| || | : |: :| ||||| || |
Db   6 IVKLDVGGKIFKTTIFTLCK-HDSMLKTMFC----TDVPVTKNEEGSVFIDRDSKHFRLI 60

Qy   86 LDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCH 136
              |::||| |: ||| | : || || | |:: | : ::|| : : |
Db   61 LNFLRDGQIALPDSDREVREVLAEASYFLLDPLIE-LCGERLEQSLNPYYH 110

RESULT 6
T33592
hypothetical protein C40A11.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
C;Accession: T33592
R;Maggi, L.; Goela, D.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid C40A11.
A;Reference number: Z21374
A;Accession: T33592
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-220 <MAG>
A;Cross-references: EMBL:AF099914; PIDN:AAC68762.1; GSPDB:GN00020; CESP:C40A11.7
A;Experimental source: strain Bristol N2; clone C40A11
C;Genetics:
A;Gene: CESP:C40A11.7
A;Map position: 2
A;Introns: 40/3; 123/3; 162/1
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC239.12

  Query Match 6.4%; Score 146.5; DB 2; Length 220;
  Best Local Similarity 38.4%; Pred. No. 0.00018;
  Matches 38; Conservative 13; Mismatches 43; Indels 5; Gaps 1;

```
Qy         26 VVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYI 85
              :|:||||| |: |  |||           |    :|   : ||:   :||||    |  :
Db          7 IVKLNVGGSVFETWKSTLTKQD-----GFFKTLVETNIPVKKDTSDCYFIDRSPKYFETV 61

Qy         86 LDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTP 124
              |:|:|    ||||   |   ||:|||:: |  || |  |
Db         62 LNYMRSGVTVLPDSEKELQELKKEAEFYLLEQLVDLCEP 100
```

RESULT 7
A41784
tumor necrosis factor-alpha-induced protein B12 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 29-Aug-1997
C;Accession: A41784
R;Wolf, F.W.; Marks, R.M.; Sarma, V.; Byers, M.G.; Katz, R.W.; Shows, T.B.;
Dixit, V.M.
J. Biol. Chem. 267, 1317-1326, 1992
A;Title: Characterization of a novel tumor necrosis factor-alpha-induced
endothelial primary response gene.
A;Reference number: A41784; MUID:92112779; PMID:1370465
A;Accession: A41784
A;Molecule type: mRNA
A;Residues: 1-348 <WOL>
A;Note: sequence extracted from NCBI backbone (NCBIN:76547, NCBIP:76550)
A;Note: it is uncertain whether Met-1 or Met-33 is the initiator
C;Genetics:
A;Gene: GDB:TNFAIP1
A;Cross-references: GDB:127514; OMIM:191161

```
A;Map position: 17q22-17q23
A;Start codon: CTG

  Query Match             6.4%;  Score 146;  DB 2;  Length 348;
  Best Local Similarity   22.2%;  Pred. No. 0.00035;
  Matches   72;  Conservative   43;  Mismatches  101;  Indels  108;  Gaps   16;

Qy         15 QGSAVPNSFPEVVELNVGGQVYF------TRHSTLISIPHSLLWKMFSPKRDTANDLAKD 68
              :|  : | :   |:||||| :|:      ||| |::         ||| :     ::  |
Db         53 KGGGLGNKY---VQLNVGGSLYYTTVRALTRHDTMLK-------AMFSGRM----EVLTD 98

Qy         69 SKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIK 128
               :|   ||| |  |  ||:||||  : || :  |   |  ||:|: :  || :
Db         99 KEGWILIDRCGKHFGTILNYLRDDTITLPQNRQEIKELMAEAKYYLIQGLVNM------- 151

Qy        129 QSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRR 188
                    | |  :|                          |:  | :          :
Db        152 ------CQSALQDKKD----------------------SYQPVCNI----PIITSLKE 177

Qy        189 VPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRF--YLKFKHLERAFDMLSECGFH 246
                |::      : | ::  : |:          |||    :|  |::|  || ||
Db        178 EERLIESSTKPVVKLLYNRSNNK--------YSYTSNSDDHL-LKNIE-LFDKLS----- 222

Qy        247 MVACNSSVTASFINQYTDDKI--WSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKEGESG 304
               :  |  |   ||     |:|  || |                       |:| |  |
Db        223 -LRFNGRVL--FIKDVIGDEICCWSFY----------------------GQGRKLAE-- 254

Qy        305 TSCNDLSTSSCDSQSEASSPQETV 328
                |  :  ::   |::   |:  :
Db        255 VCCTSIVYATEKKQTKVEFPEARI 278


RESULT 8
T33590
hypothetical protein C40A11.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
C;Accession: T33590
R;Maggi, L.; Goela, D.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid C40A11.
A;Reference number: Z21374
A;Accession: T33590
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-179 <MAG>
A;Cross-references: EMBL:AF099914; PIDN:AAC68757.1; GSPDB:GN00020; CESP:C40A11.6
A;Experimental source: strain Bristol N2; clone C40A11
C;Genetics:
A;Gene: CESP:C40A11.6
A;Map position: 2
A;Introns: 40/3; 123/3
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC239.12

  Query Match             6.4%;  Score 145.5;  DB 2;  Length 179;
  Best Local Similarity   38.4%;  Pred. No. 0.00016;
  Matches   38;  Conservative   13;  Mismatches   43;  Indels    5;  Gaps    1;
```

```
Qy          26 VVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYI 85
               :|:|||||  |: |  |||           |    :|   : ||:   :||||    |  :
Db           7 IVKLNVGGSVFETWKSTLTKQD-----GFFKTLIETNVPVKKDTSDCYFIDRSPKYFETV 61

Qy          86 LDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTP 124
               |:|:|    ||||   |   ||:|||:: |  || |  |
Db          62 LNYMRSGVTVLPDSEKELQELKKEAEFYLLEHLVDLCEP 100


RESULT 9
T31997
hypothetical protein B0281.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
C;Accession: T31997
R;Pauley, A.; Scheet, P.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid B0281.
A;Reference number: Z21109
A;Accession: T31997
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-212 <PAU>
A;Cross-references: EMBL:AF016666; PIDN:AAB66085.1; GSPDB:GN00020; CESP:B0281.6
A;Experimental source: strain Bristol N2; clone B0281
C;Genetics:
A;Gene: CESP:B0281.6
A;Map position: 2
A;Introns: 40/3; 121/3; 160/1
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC239.12

  Query Match             6.3%;  Score 144;  DB 2;  Length 212;
  Best Local Similarity   38.5%;  Pred. No. 0.00027;
  Matches   45;  Conservative   10;  Mismatches   44;  Indels   18;  Gaps    4;

Qy          22 SFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFL 81
               |   :|:||||| |: |  |||    |  ::|        | |   ||   |||||
Db           3 SSESIVKLNVGGTVFVTLKSTLTK--HHGIFKALVKTEMPAED--GDS---FFIDRSPKH 55

Qy          82 FRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLL-----------TPDEI 127
               |  :|:|:|   | |||   |   |||||||: |  |  |             | ||:
Db          56 FETVLNYIRSGDVDLPDSENELKELKREAEYYSLEKLATLCQSSMPKIKSYKTADEL 112


RESULT 10
T26685
hypothetical protein F18A11.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26685
R;Wallis, J.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z20253
A;Accession: T26685
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
```

```
A;Residues: 1-373 <WIL>
A;Cross-references: EMBL:AL032639; PIDN:CAA21638.1; GSPDB:GN00020; CESP:F18A11.5
A;Experimental source: clone Y38F1A
C;Genetics:
A;Gene: CESP:F18A11.5
A;Map position: 2
A;Introns: 7/3; 44/3; 99/3; 152/2; 198/3; 223/1

  Query Match             5.8%;  Score 131.5;  DB 2;  Length 373;
  Best Local Similarity   32.5%;  Pred. No. 0.0059;
  Matches   40;  Conservative   20;  Mismatches   40;  Indels   23;  Gaps    4;

Qy          8 SRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAK 67
              |  : :| ||    :  | | |||||: : |  :||  :  ::|  | | :  | :::
Db          7 SMTFSQEGGS----NLSERVLLNVGGKKFETTVATLTRVSDTVLAVMVSDRWKTGDEI-- 60

Qy         68 DSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKG------RLKREAEYFQLPDLVKL 121
                    |||||   |  :|:||||      |||           |||||  :: :| | ::
Db         61 ------FIDRDPKHFGKVLNYLRD-----GDHFVAPSDTEACDELKREAHFYNMPFLAEM 109

Qy        122 LTP 124
               |
Db        110 CMP 112


RESULT 11
T32070
hypothetical protein F22E5.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
C;Accession: T32070
R;Graves, T.; Wohldmann, P.; Clarke, K.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid F22E5.
A;Reference number: Z21119
A;Accession: T32070
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-231 <GRA>
A;Cross-references: EMBL:AF016681; PIDN:AAB66172.1; GSPDB:GN00020; CESP:F22E5.6
A;Experimental source: strain Bristol N2; clone F22E5
C;Genetics:
A;Gene: CESP:F22E5.6
A;Map position: 2
A;Introns: 40/3; 125/3; 170/1
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC239.12

  Query Match             5.4%;  Score 122.5;  DB 2;  Length 231;
  Best Local Similarity   24.2%;  Pred. No. 0.017;
  Matches   46;  Conservative   21;  Mismatches   66;  Indels   57;  Gaps    4;

Qy         25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRY 84
              | : ||:|| :: |  |||           |    :|   : ||     ||||    |
Db          6 EKIRLNIGGTIFETSKSTLTKFD-----GFFKTLLETDIPIQKDDSNCIFIDRSPRHFEK 60

Qy         85 ILDYLRDRQVV--LPDHFPEKGRLKREAEYFQLPDLVK---------------------- 120
              ||:||||   |  ||:   |   : :||::: |  |::
```

```
Db         61 ILNYLRDGADVDLLPESEKEVREILKEAQFYLLEGLMELCKRSSCKIRTFESYHHLLKLI 120

Qy        121 ------------LLTPDEIKQSPDEFCHSDFEDASQGS----------------DTRICP 152
                          |:  : |   |: |   || :  ||                  :|
Db        121 AEAGKPVLVMFYLVKDNRIVHVPNNFEFLDFLEKHQGKLDIYFSEFGQKKESPYETTHQN 180

Qy        153 PSSLLPADRK 162
              ||  ||  |:
Db        181 PSQFLPPGRE 190
```

RESULT 12
T33589
hypothetical protein C40A11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T33589
R;Maggi, L.; Goela, D.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid C40A11.
A;Reference number: Z21374
A;Accession: T33589
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-236 <MAG>
A;Cross-references: EMBL:AF099914; PIDN:AAC68765.1; GSPDB:GN00020; CESP:C40A11.3
A;Experimental source: strain Bristol N2; clone C40A11
C;Genetics:
A;Gene: CESP:C40A11.3
A;Map position: 2
A;Introns: 40/3; 124/3; 163/1; 196/3

  Query Match   5.4%; Score 122.5; DB 2; Length 236;
  Best Local Similarity   35.4%; Pred. No. 0.018;
  Matches   34; Conservative   15; Mismatches   42; Indels   5; Gaps   1;

```
Qy         26 VVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYI 85
              :: ||:|| |: |  :||  |        |    ::   | ||     ||||    |  |
Db          7 IMMLNIGGTVFHTSKATLTGIN-----GFFKMLLESDIPLHKDESNCIFIDRSPKHFDVI 61

Qy         86 LDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKL 121
              |::|||  | ||:   |   ::|||::: |  || |
Db         62 LNFLRDGDVDLPELEKEVKEVRREAQFYLLDGLVYL 97
```

RESULT 13
T25978
hypothetical protein ZC239.15 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T25978
R;Wu, X.; Kramer, J.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid ZC239.
A;Reference number: Z20117
A;Accession: T25978
A;Status: preliminary; translated from GB/EMBL/DDBJ

```
A;Molecule type: DNA
A;Residues: 1-246 <WUX>
A;Cross-references: EMBL:U80842; PIDN:AAB37955.1; GSPDB:GN00020; CESP:ZC239.15
A;Experimental source: strain Bristol N2; clone ZC239
C;Genetics:
A;Gene: CESP:ZC239.15
A;Map position: 2
A;Introns: 37/3; 127/3
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC239.12

  Query Match             5.3%;  Score 121.5;  DB 2;  Length 246;
  Best Local Similarity   32.2%;  Pred. No. 0.023;
  Matches   38;  Conservative   19;  Mismatches   52;  Indels    9;  Gaps    3;

Qy         25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRY 84
              | |:|:||| :: |  |||           |    ::   |  |  |  ||||    |
Db          3 ETVKLDVGGTIFKTSRSTLTKFN-----GFFKTMLESDIGLKIDESGSIFIDRSPKNFDL 57

Qy         85 ILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPD-EIKQSPD---EFCHSD 138
              ||:::||  ||||:   :   |  ||::: |  |::|     |: ::|     |  ||
Db         58 ILNFMRDGDVVLPNCELKLKELLVEAQFYLLDGLIELCNSKIELVEAPKIKLRFIESD 115


RESULT 14
T21630
hypothetical protein F32B4.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T21630
R;White, S.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19452
A;Accession: T21630
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-277 <WIL>
A;Cross-references: EMBL:Z81522; PIDN:CAB04230.1; GSPDB:GN00019; CESP:F32B4.5
A;Experimental source: clone F32B4
C;Genetics:
A;Gene: CESP:F32B4.5
A;Map position: 1
A;Introns: 131/3; 237/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F32B4.5

  Query Match             5.2%;  Score 119;  DB 2;  Length 277;
  Best Local Similarity   24.1%;  Pred. No. 0.042;
  Matches   58;  Conservative   28;  Mismatches   75;  Indels   80;  Gaps   10;

Qy         33 GQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYILDYLR-- 90
              |    |  :||   | |||         |: |   ||        |  : | ::: ||
Db         69 GATISTTRATLQRAPQSLL--------ATSPDATSDS--------DDKIVRILVEALRRS 112

Qy         91 DRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQGSDTRI 150
              |  ::: : | :  ||  ||:   |   |:   |  |  |    ||:        |  ||
Db        113 DMSIIVSESFDQWARLAVEAKRLGLISFVEAACPSTISIS----CHAAL------STGRI 162

Qy        151 CPPSSLLPADRKWGFITVGYRGSCTLGR----------EGQADAKF-------------- 186
```

```
              |  :     ||     : :    | |:          :|   : |
Db        163 NPEVTF----RK--VHNIHFMAQKTTGKAFASSNPEPVKGTTTSPFFLLSFFFPFFCSFL 216

Qy        187 -------------------RRVPRILVCGRISLAKEVFGETLNESRD---PDRAPERYTS 224
                                | ||:| |:: : : |||::||| ||    |   :||||
Db        217 LRFSPINFPLLLLMNTAIGEYVLRIVVSGKVIMCRAVFGDSLNECRDGGGTDFEMDRYTS 276

Qy        225 R 225
              |
Db        277 R 277
```

RESULT 15
T32065
hypothetical protein F22E5.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32065
R;Graves, T.; Wohldmann, P.; Clarke, K.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid F22E5.
A;Reference number: Z21119
A;Accession: T32065
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-134 <GRA>
A;Cross-references: EMBL:AF016681; PIDN:AAB66174.1; GSPDB:GN00020; CESP:F22E5.8
A;Experimental source: strain Bristol N2; clone F22E5
C;Genetics:
A;Gene: CESP:F22E5.8
A;Map position: 2
A;Introns: 37/3

  Query Match   5.1%; Score 115.5; DB 2; Length 134;
  Best Local Similarity   35.1%; Pred. No. 0.031;
  Matches   34; Conservative   16; Mismatches   42; Indels   5; Gaps   2;

```
Qy         25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRY 84
              | |:|:||| :: |  |||    :  |  |     ::   |  |  |  ||||    |
Db          3 ETVQLDVGGTIFKTSKSTLTKF-NGFLKIML----ESDIGLKIDESGSIFIDRSPKHFDL 57

Qy         85 ILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKL 121
              ||:::||  ||||        |  ||::: | :|::|
Db         58 ILNFMRDGDVVLPSCELTVKELLAEAQFYLLDELIEL 94
```

Search completed: January 29, 2004, 02:55:49
Job time : 31 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 28, 2004, 23:02:20 ; Search time 18 Seconds
(without alignments)
1118.191 Million cell updates/sec

Title: US-10-056-884A-2
Perfect score: 2284
Sequence: 1 MALSGNCSRYYPREQGSAVP.....DRFPERKHPWQSELLRKYHL 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	146.5	6.4	265	1	Y176_HUMAN	Q14681 homo sapien
2	146	6.4	316	1	TNP1_HUMAN	Q13829 homo sapien
3	105	4.6	1504	1	DPOZ_YEAST	P14284 saccharomyc
4	104.5	4.6	1176	1	NIR_NEUCR	P38681 neurospora
5	104	4.6	490	1	CIKL_DROME	P17971 drosophila
6	103.5	4.5	140	1	YR43_CAEEL	Q09389 caenorhabdi
7	102	4.5	491	1	KCS3_RAT	O88759 rattus norv
8	101.5	4.4	1537	1	DNM1_CHICK	Q92072 gallus gall
9	100	4.4	491	1	KCS3_HUMAN	Q9bq31 homo sapien
10	100	4.4	737	1	ADDA_HUMAN	P35611 homo sapien
11	99	4.3	491	1	KCS3_RABIT	Q9tt17 oryctolagus
12	98	4.3	329	1	IRF1_MOUSE	P15314 mus musculu
13	98	4.3	825	1	SWI3_YEAST	P32591 saccharomyc
14	97.5	4.3	1213	1	FMN_CHICK	Q05858 gallus gall
15	96.5	4.2	1186	1	PKCB_HUMAN	Q9ulu4 homo sapien
16	96.5	4.2	3695	1	LMA5_HUMAN	O15230 homo sapien
17	95	4.2	1023	1	STR8_HUMAN	Q92502 homo sapien

18	95	4.2	3390	1	POLG_DEN3	P27915	d genome po
19	94	4.1	548	1	CNE2_MOUSE	P59108	mus musculu
20	93	4.1	601	1	YE06_SCHPO	O13803	schizosacch
21	92	4.0	352	1	P53_ORYLA	P79820	oryzias lat
22	92	4.0	768	1	RGL1_MOUSE	Q60695	mus musculu
23	91.5	4.0	3767	1	MUA3_CAEEL	P34576	caenorhabdi
24	91	4.0	1275	1	GNRP_HUMAN	Q13972	homo sapien
25	91	4.0	1969	1	Z292_HUMAN	O60281	homo sapien
26	91	4.0	3083	1	POLG_ZYMVS	O36979	z genome po
27	90	3.9	357	1	CHLI_SYNY3	P51634	synechocyst
28	90	3.9	793	1	ATK1_ARATH	Q07970	arabidopsis
29	89.5	3.9	640	1	ELM1_YEAST	P32801	saccharomyc
30	89.5	3.9	1015	1	DNL3_MOUSE	P97386	mus musculu
31	89.5	3.9	5038	1	PCLO_MOUSE	Q9qyx7	mus musculu
32	89	3.9	523	1	CIK3_HUMAN	P22001	homo sapien
33	89	3.9	683	1	YKB7_YEAST	P34243	saccharomyc
34	89	3.9	705	1	YNP9_CAEEL	P34562	caenorhabdi
35	89	3.9	2476	1	ATRX_MOUSE	Q61687	mus musculu
36	88.5	3.9	283	1	YQVW_CAEEL	Q17439	caenorhabdi
37	88.5	3.9	538	1	Z306_HUMAN	Q9brr0	homo sapien
38	88.5	3.9	625	1	CIKG_RAT	Q63734	rattus norv
39	88	3.9	3829	1	SACS_HUMAN	Q9nzj4	homo sapien
40	87.5	3.8	477	1	GATB_MYCPN	P75533	mycoplasma
41	87.5	3.8	486	1	WHI2_YEAST	P12611	saccharomyc
42	87.5	3.8	664	1	PLB1_YEAST	P39105	saccharomyc
43	87	3.8	249	1	YAT6_RHOBL	P05449	rhodopseudo
44	87	3.8	345	1	YAYE_SCHPO	Q10221	schizosacch
45	87	3.8	1565	1	DMN_HUMAN	O15061	homo sapien

ALIGNMENTS

```
RESULT 1
Y176_HUMAN
ID   Y176_HUMAN     STANDARD;      PRT;   265 AA.
AC   Q14681;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein KIAA0176 (Fragment).
GN   KIAA0176.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RX   MEDLINE=96281124; PubMed=8724849;
RA   Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;
RT   "Prediction of the coding sequences of unidentified human genes. V.
RT   The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced by
RT   analysis of cDNA clones from human cell line KG-1.";
RL   DNA Res. 3:17-24(1996).
CC   -!- SIMILARITY: Contains 1 BTB/POZ domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; D79998; BAA11493.1; -.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR003131; K_tetra.
DR   Pfam; PF02214; K_tetra; 1.
DR   SMART; SM00225; BTB; 1.
DR   PROSITE; PS50097; BTB; FALSE_NEG.
KW   Hypothetical protein.
FT   NON_TER       1      1
FT   DOMAIN       74    174       BTB.
SQ   SEQUENCE   265 AA;  28801 MW;  5C7455CCBBEE8924 CRC64;

  Query Match             6.4%;  Score 146.5;  DB 1;  Length 265;
  Best Local Similarity   30.2%;  Pred. No. 0.00026;
  Matches   51;  Conservative   25;  Mismatches   68;  Indels   25;  Gaps    8;

Qy         27 VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYIL 86
              | |||||  : |   ||   | | | ::   : |   |  ||  | : ||||   |  ||
Db         76 VRLNVGGTYFVTTRQTLGREPKSFLCRLCC-QEDPELDSDKDETGAYLIDRDPTYFGPIL 134

Qy         87 DYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQGS 146
              :|||  ::::     |:| |: |||:: :  ||:|:  : |: : :          |||
Db        135 NYLRHGKLIITKELAEEGVLE-EAEFYNIASLVRLV-KERIRDNENR--------TSQGP 184

Qy        147 DTRI-----CPPSSLL----PADRKWGF---ITVGYRGSCTLGREGQAD 183
                 :     |    |          | |   |::|   |   | | ||:
Db        185 VKHVYRVLQCQEEELTQMVSTMSDGWKFEQLISIG--SSYNYGNEDQAE 231


RESULT 2
TNP1_HUMAN
ID   TNP1_HUMAN     STANDARD;      PRT;   316 AA.
AC   Q13829;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Tumor necrosis factor, alpha-induced protein 1, endothelial (B12
DE   protein).
GN   TNFAIP1 OR EDP1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Endothelial cells;
RX   MEDLINE=92112779; PubMed=1370465;
RA   Wolf F.W., Marks R.M., Sarma V., Byers M.G., Katz R.W., Shows T.B.,
RA   Dixit V.M.;
RT   "Characterization of a novel tumor necrosis factor-alpha-induced
```

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RT   endothelial primary response gene.";
RL   J. Biol. Chem. 267:1317-1326(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA   Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- INDUCTION: BY TNF-ALPHA, INTERLEUKIN-1 BETA AND LIPOPOLYSACCHARIDE
CC       (LPS).
CC   -!- SIMILARITY: Contains 1 BTB/POZ domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M80783; AAA58385.1; -.
DR   EMBL; AY065346; AAL38649.1; -.
DR   EMBL; BC001643; AAH01643.1; -.
DR   EMBL; BC001949; AAH01949.1; -.
DR   Genew; HGNC:11894; TNFAIP1.
DR   MIM; 191161; -.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR003131; K_tetra.
DR   Pfam; PF02214; K_tetra; 1.
DR   SMART; SM00225; BTB; 1.
DR   PROSITE; PS50097; BTB; 1.
FT   DOMAIN       28     96       BTB.
SQ   SEQUENCE   316 AA;  36204 MW;  D20B810A00507DCF CRC64;
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  Query Match             6.4%;  Score 146; DB 1;  Length 316;
  Best Local Similarity   22.2%;  Pred. No. 0.00036;
  Matches   72;  Conservative   43;  Mismatches  101;  Indels  108;  Gaps   16;

Qy         15 QGSAVPNSFPEVVELNVGGQVYF------TRHSTLISIPHSLLWKMFSPKRDTANDLAKD 68
              :|  : | :   |:||||| :|:      ||| |::      ||| :     ::  |
Db         21 KGGGLGNKY---VQLNVGGSLYYTTVRALTRHDTMLK-------AMFSGRM----EVLTD 66

Qy         69 SKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIK 128
              :|   ||| |  |  ||:||||  : || :  |   |  ||:|: :  || :
Db         67 KEGWILIDRCGKHFGTILNYLRDDTITLPQNRQEIKELMAEAKYYLIQGLVNM------- 119

Qy        129 QSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRR 188
                  | |  :|                          |:  | :          :
Db        120 ------CQSALQDKKD-----------------------SYQPVCNI----PIITSLKE 145

Qy        189 VPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRF--YLKFKHLERAFDMLSECGFH 246
                |::      : | ::  : |:          |||    :|  |::|  || ||
Db        146 EERLIESSTKPVVKLLYNRSNNK--------YSYTSNSDDHL-LKNIE-LFDKLS----- 190

Qy        247 MVACNSSVTASFINQYTDDKI--WSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKEGESG 304
               :  |  |   ||     |:|  || |                          |:| |  |
Db        191 -LRFNGRVL--FIKDVIGDEICCWSFY----------------------GQGRKLAE-- 222

Qy        305 TSCNDLSTSSCDSQSEASSPQETV 328
               |  :  ::   |::   |:  :
Db        223 VCCTSIVYATEKKQTKVEFPEARI 246


RESULT 3
DPOZ_YEAST
ID   DPOZ_YEAST     STANDARD;      PRT;  1504 AA.
AC   P14284;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   DNA polymerase zeta catalytic subunit (EC 2.7.7.7).
GN   REV3 OR PSO1 OR YPL167C OR P2535.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90008808; PubMed=2676986;
RA   Morrison A., Christensen R.B., Alley J., Beck A.K., Bernstine E.G.,
RA   Lemontt J.F., Lawrence C.W.;
RT   "REV3, a Saccharomyces cerevisiae gene whose function is required for
RT   induced mutagenesis, is predicted to encode a nonessential DNA
RT   polymerase.";
RL   J. Bacteriol. 171:5659-5667(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c / AB972;
RX   MEDLINE=97103777; PubMed=8948103;
RA   Purnelle B., Coster F., Goffeau A.;
RT   "The sequence of 55 kb on the left arm of yeast chromosome XVI
```

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RT   identifies a small nuclear RNA, a new putative protein kinase and two
RT   new putative regulators.";
RL   Yeast 12:1483-1492(1996).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c / AB972;
RX   MEDLINE=97313271; PubMed=9169875;
RA   Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W.,
RA   Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
RA   Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
RA   Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA   Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,
RA   Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
RA   Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,
RA   Hunicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,
RA   Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA   Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,
RA   Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
RA   Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M.,
RA   Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,
RA   Urrestarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
RA   Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,
RA   Zhong W.W., Zollner A., Vo D.H., Hani J.;
RT   "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
RL   Nature 387:103-105(1997).
CC   -!- FUNCTION: REQUIRED FOR INDUCED MUTAGENESIS, IT IS A NONESSENTIAL
CC       DNA POLYMERASE. IT MAY FUNCTION IN TRANSLESION SYNTHESIS.
CC       TRANSLESION SYNTHESIS IN S.CEREVISIAE MAY USE A SPECIALIZED DNA
CC       POLYMERASE THAT IS NOT REQUIRED FOR OTHER DNA REPLICATIVE
CC       PROCESSES.
CC   -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC       + {DNA}(N).
CC   -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC   -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-B FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M29683; AAA34968.1; -.
DR   EMBL; X96770; CAA65554.1; -.
DR   EMBL; Z73523; CAA97873.1; -.
DR   PIR; A33602; A33602.
DR   SGD; S0006088; REV3.
DR   InterPro; IPR006172; DNA_pol_B.
DR   InterPro; IPR006134; DNA_pol_B_dom.
DR   InterPro; IPR006133; DNA_pol_B_exo.
DR   Pfam; PF00136; DNA_pol_B; 1.
DR   Pfam; PF03104; DNA_pol_B_exo; 1.
DR   PRINTS; PR00106; DNAPOLB.
DR   SMART; SM00486; POLBc; 1.
DR   PROSITE; PS00116; DNA_POLYMERASE_B; 1.
KW   Transferase; DNA-directed DNA polymerase; DNA replication;
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KW   DNA-binding; DNA repair; Nuclear protein; Zinc-finger.
FT   ZN_FING    1398   1417       C4-TYPE (POTENTIAL).
FT   ZN_FING    1446   1473       C4-TYPE (POTENTIAL).
SQ   SEQUENCE   1504 AA;  172956 MW;  54C2C6B664F734F5 CRC64;

  Query Match             4.6%;  Score 105;  DB 1;  Length 1504;
  Best Local Similarity   20.2%;  Pred. No. 4.5;
  Matches  111;  Conservative   67;  Mismatches  186;  Indels  186;  Gaps   26;

Qy         12 PREQGSAVPN-----SFP-------------EVVELNVGGQVYFT---RHSTLISIPHSL 50
              |  | | |||     : |               : :   ||:  |   ||     :  :|
Db         49 PLNQFSQVPNIRVFGALPTGHQVLCHVHGILPYMFIKYDGQITDTSTLRHQRCAQVHKTL 108

Qy         51 LWKM---FSPKRDTANDLAKDSKGR--------------FFIDRDGFLFRY--------- 84
                |:   |  |:|  :||| |  |                 |:    |:   |
Db        109 EVKIRASFKRKKDDKHDLAGDKLGNLNFVADVSVVKGIPFYGYHVGWNLFYKISLLNPSC 168

Qy         85 ---ILDYLRDRQV------VLPDHFPEKGRLKREAE--------------YFQLP----- 116
                | : :|| ::      :   | |    |:  |:              ||: |
Db        169 LSRISELIRDGKIFGKKFEIYESHIPY--LLQWTADFNLFGCSWINVDRCYFRSPVLNSI 226

Qy        117 -DLVKLLTPDEIKQSPDEFC--------HSDFEDASQG-SDTRICPP-----SSLLPADR 161
               |: ||   |:::   | ||          ||     |  :  | |         |   |
Db        227 LDIDKLTINDDLQLLLDRFCDFKCNVLSRRDFPRVGNGLIEIDILPQFIKNREKLQHRDI 286

Qy        162 KWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVFGE--------TLNESR 213
                |:                 |   :  | |   :| |:::  |         :| | :
Db        287 HHDFL-----------------EKLGDISDIPVKPYVSSARDMINELTMQREELSLKEYK 329

Qy        214 DPDRAPERYTS-----------RFYLKFKHLERAFDMLSECGFHMVACNSSVTA------ 256
              :|    :|: |            || | :|    ||       : :  |   :|
Db        330 EPPET-KRHVSGHQWQSSGEFEAFYKKAQHKTSTFDGQIPNFENFIDKNQKFSAINTPYE 388

Qy        257 -----------------SFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDK 299
                              |  ::  ||:: :|:|||               |   |   :
Db        389 ALPQLWPRLPQIEINNNSMQDKKNDDQVNASFTEYEI-------------CGVDN---EN 432

Qy        300 EGESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEM 359
              ||  |::    | |    :| ||    |::    |:  |  |::  :      : |
Db        433 EGVKGSNIKSRSYSWL-PESIASPKDSTILLDHQTKYHN--TINFSM---DCAMTQNMAS 486

Qy        360 RRKSDLLRILTSGSRESNMSSKKKAVK-------EKLSIEEELEKCIQDFLKKKIPDRFP 412
              :||   ||   | :: | :| |:| |        ::  :  |     || | |   : ||
Db        487 KRK---LRSSVSANKTSLLSRKRKKVMAAGLRYGKRAFVYGEPPFGYQDILNKLEDEGFP 543

Qy        413 --ERKHPWQS 420
                : | |: |
Db        544 KIDYKDPFFS 553


RESULT 4
NIR_NEUCR
ID   NIR_NEUCR      STANDARD;      PRT;  1176 AA.
AC   P38681;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
```

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DE   Nitrite reductase [NAD(P)H] (EC 1.7.1.4).
GN   NIT-6.
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=74-OR23-1A / FGSC 987;
RX   MEDLINE=93224461; PubMed=8096840;
RA   Exley G.E., Colandene J.D., Garrett R.H.;
RT   "Molecular cloning, characterization, and nucleotide sequence of
RT   nit-6, the structural gene for nitrite reductase in Neurospora
RT   crassa.";
RL   J. Bacteriol. 175:2379-2392(1993).
CC   -!- CATALYTIC ACTIVITY: Ammonium hydroxide + 3 NAD(P)(+) + H(2)O =
CC       nitrite + 3 NAD(P)H.
CC   -!- COFACTOR: THIS ENZYME IS A FAD FLAVOPROTEIN THAT ALSO CONTAINS
CC       A SIROHEME AND ONE 4FE-4S IRON-SULFUR CENTER.
CC   -!- PATHWAY: Nitrate assimilation (denitrification); second step.
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- INDUCTION: By nitrate.
CC   -!- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN
CC       FOUND IN NITRITE REDUCTASES (EC 1.7.1.4 AND EC 1.7.7.1) AND
CC       SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; L07391; -; NOT_ANNOTATED_CDS.
DR   PIR; A49848; A49848.
DR   InterPro; IPR001327; FAD_pyr_redox.
DR   InterPro; IPR006066; Nir_Si.
DR   InterPro; IPR006067; Nir_Sir_4Fe4S.
DR   InterPro; IPR005117; Nir_sir_fer.
DR   InterPro; IPR005806; Rieske_dom.
DR   Pfam; PF04324; fer2_BFD; 1.
DR   Pfam; PF01077; NIR_SIR; 1.
DR   Pfam; PF03460; NIR_SIR_ferr; 1.
DR   Pfam; PF00070; pyr_redox; 1.
DR   Pfam; PF00355; Rieske; 1.
DR   PRINTS; PR00368; FADPNR.
DR   PRINTS; PR00397; SIROHAEM.
DR   PROSITE; PS00365; NIR_SIR; 1.
KW   Oxidoreductase; FAD; Flavoprotein; Metal-binding; Iron-sulfur; Iron;
KW   4Fe-4S; Nitrate assimilation; Heme; NADP.
FT   NP_BIND      26     60       FAD (POTENTIAL).
FT   NP_BIND     183    215       NAD(P)H (POTENTIAL).
FT   METAL       717    717       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       723    723       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       757    757       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT   METAL       761    761       IRON-SULFUR (4FE-4S) (BY SIMILARITY).
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FT   METAL       761    761       IRON (SIROHEME AXIAL LIGAND) (BY
FT                                SIMILARITY).
FT   DOMAIN      998   1054       PRO/SER-RICH.
SQ   SEQUENCE   1176 AA;  127367 MW;  FFC7DCE66F80C710 CRC64;

  Query Match             4.6%;  Score 104.5;  DB 1;  Length 1176;
  Best Local Similarity   19.8%;  Pred. No. 3.5;
  Matches   85;  Conservative   44;  Mismatches  122;  Indels  179;  Gaps   21;

Qy         69 SKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKRE------------------ 109
              | | || ||||                  |   | |  |:||
Db        385 SFGDFFADRDG-----------------PKELPPK--LRRELKKSGGKAEVKALTYKDPF 425

Qy        110 -------------------------AEYFQLPDLVKL-----LTPDEI----KQSPDEFC 135
                                       :| :|  |||      : | ::    |:| |:
Db        426 LSVYKKYIFTSDGKYLLGGMMIGDTTDYVRLVPLVKTHKELDVPPSQLILGAKKSGDDNG 485

Qy        136 HSDFEDASQGSDTRICPPSSLLPAD----RKWGFIT-VGYRGSCTLGREGQADAKFRRVP 190
                |  |     ||:||   ::  ||     | |  | :|   |||    |
Db        486 DDDLPD-----DTQICSCHNVTKADLVAPLKSGECTSLGDLKSCTKAGTG---------- 530

Qy        191 RILVCGR-ISLAKEVFGETL----NESRDP--DRAPERYTSRFY--LKFKHLERAFDMLS 241
                 ||  : |   :|  |:     | ::      ||   :  |  :  | |    |::
Db        531 ----CGGCMPLVTSIFNRTMASLGTEVKNNLCPHFPEYSRADLYNIISVKRLRTLPDVMR 586

Qy        242 ECG-----FHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGK 296
              | |          ||  :: : | :      :|: :            ||:|      :|
Db        587 EAGADADSLGCEACKPAIASIFAS------LWNDHV----------MSPAH------HGL 624

Qy        297 GDKEGESGTSCNDLSTSSCDSQSEAS--SPQETVICGPVTRQTNIQTLDRPIKKGPVQLI 354
               |       :     | |   :  |   :|:: :: | | :: |: |
Db        625 QDTNDRFMGNIQRNGTFSVVPRVAAGEITPEKLIVIGEVAKEYNLYTK------------ 672

Qy        355 QQSEMRRKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLK--KKIPDRFP 412
                          :| | |     :||                  || ||  ||: |
Db        673 --------------ITGGQRIDMFGAKK----------------QDLLKIWKKLVDAGM 701

Qy        413 ERKHPWQSEL 422
              |  | :   |
Db        702 ESGHAYAKSL 711


RESULT 5
CIKL_DROME
ID   CIKL_DROME     STANDARD;      PRT;   490 AA.
AC   P17971; Q9VW11;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Potassium voltage-gated channel protein Shal (Shal2).
GN   SHAL OR SHAL2 OR CG9262.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
```

RP   SEQUENCE FROM N.A.
RX   MEDLINE=90239553; PubMed=2333511;
RA   Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
RT   "K+ current diversity is produced by an extended gene family
RT   conserved in Drosophila and mouse.";
RL   Science 248:599-603(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90245668; PubMed=2336395;
RA   Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
RT   "Shal, Shab, and Shaw: three genes encoding potassium channels in
RT   Drosophila.";
RL   Nucleic Acids Res. 18:2173-2174(1990).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
CC   -!- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC   ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED

```
CC       CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC       MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC       WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC       GRADIENT. MAY PLAY A ROLE IN THE NERVOUS SYSTEM AND IN THE
CC       REGULATION OF BEATING FREQUENCY IN PACEMAKER CELLS.
CC   -!- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=P17971-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P17971-2; Sequence=Not described;
CC   -!- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC       RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC       IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC       TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC   -!- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
CC       IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC       EVERY THIRD POSITION.
CC   -!- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. SHAL
CC       SUBFAMILY.
CC   -!- CAUTION: Ref.3 sequence differs from that shown due to erroneous
CC       gene model prediction.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M32660; AAA28895.1; -.
DR   EMBL; AE003516; AAF49144.1; ALT_SEQ.
DR   PIR; A35312; A35312.
DR   FlyBase; FBgn0005564; Shal.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR003131; K_tetra.
DR   InterPro; IPR003968; Kv_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR003975; Shal_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF02214; K_tetra; 1.
DR   PRINTS; PR00169; KCHANNEL.
DR   PRINTS; PR01491; KVCHANNEL.
DR   PRINTS; PR01497; SHALCHANNEL.
DR   SMART; SM00225; BTB; 1.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium transport; Potassium; Transmembrane;
KW   Glycoprotein; Multigene family; Alternative splicing.
FT   TRANSMEM    186    204       SEGMENT S1.
FT   TRANSMEM    229    250       SEGMENT S2.
FT   TRANSMEM    261    282       SEGMENT S3.
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FT   TRANSMEM    290    308       SEGMENT S4.
FT   TRANSMEM    324    345       SEGMENT S5.
FT   TRANSMEM    385    406       SEGMENT S6.
FT   CARBOHYD     46     46       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    350    350       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    353    353       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    408    408       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   490 AA;  55918 MW;  E178E1C89B07DA74 CRC64;

  Query Match             4.6%;  Score 104;  DB 1;  Length 490;
  Best Local Similarity   27.7%;  Pred. No. 1.2;
  Matches   36;  Conservative   27;  Mismatches   41;  Indels   26;  Gaps    7;

Qy         25 EVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRY 84
              | : :|| |: : |  :||   | :||    | :|:   |  :| |  :| |||  :||:
Db         41 EKLLINVSGRRFETWRNTLEKYPDTLLG---SNEREFFYD--EDCK-EYFFDRDPDIFRH 94

Qy         85 ILDYLRDRQVVLPDHFPEKGRL---KREAEYFQ-LPDLVKLLTPDEIKQSPDEFCHSDFE 140
              ||:| |  ::    |:|:   |     |  :|  :||::             : |: |:
Db         95 ILNYYRTGKL----HYPKHECLTSYDEELAFFGIMPDVI------------GDCCYEDYR 138

Qy        141 DASQGSDTRI 150
              |  : :  |:
Db        139 DRKRENAERL 148


RESULT 6
YR43_CAEEL
ID   YR43_CAEEL     STANDARD;      PRT;   140 AA.
AC   Q09389;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical 16.3 kDa protein F47D12.3 in chromosome III.
GN   F47D12.3.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Taich A.;
RL   Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U22831; AAK20065.1; -.
DR   PIR; A88479; A88479.
DR   WormPep; F47D12.3; CE01947.
DR   InterPro; IPR003131; K_tetra.
```

```
DR   Pfam; PF02214; K_tetra; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   140 AA;  16301 MW;  E4866BD5F2A6CA15 CRC64;

  Query Match             4.5%;  Score 103.5;  DB 1;  Length 140;
  Best Local Similarity   27.3%;  Pred. No. 0.25;
  Matches   42;  Conservative   24;  Mismatches   55;  Indels   33;  Gaps    5;

Qy          3 LSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTL-------------ISIPHS 49
              || ||   :               : | |||::|  :  ||             : :  :
Db          5 LSFNCEDAW---------------LNLFVGGEMYPVQVKTLMNPTTCGSYFRDVVKVSDA 49

Qy         50 LLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVV-LPDHFPEKGRLKR 108
               : |:   : |||       | |  ||||| |||::| |||: ::  |||       |
Db         50 AI-KVRGVQWDTA---PNHIKFRVDIDRDGVLFRHVLQYLRNGKLTSLPDDIFTLESLVA 105

Qy        109 EAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDA 142
              |||:| |    ::|     | :     :: :||:
Db        106 EAEFFGLEKYREMLKKKLWKLTGKRQYYACYEDS 139


RESULT 7
KCS3_RAT
ID   KCS3_RAT       STANDARD;      PRT;   491 AA.
AC   O88759; O54900;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Potassium voltage-gated channel subfamily S member 3 (Potassium
DE   channel Kv9.3) (Delayed-rectifier K+ channel alpha subunit 3).
GN   KCNS3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain, and Kidney;
RX   MEDLINE=98031889; PubMed=9362476;
RA   Patel A.J., Lazdunski M., Honore E.;
RT   "Kv2.1/Kv9.3, a novel ATP-dependent delayed-rectifier K+ channel in
RT   oxygen-sensitive pulmonary artery myocytes.";
RL   EMBO J. 16:6615-6625(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98369652; PubMed=9704029;
RA   Stocker M., Kerschensteiner D.;
RT   "Cloning and tissue distribution of two new potassium channel
RT   alpha-subunits cloned from rat brain.";
RL   Biochem. Biophys. Res. Commun. 248:927-934(1998).
CC   -!- FUNCTION: Potassium channel subunit. Modulates channel activity
CC       and shifts the activation threshold of KCNB1 to more negative
CC       values.
CC   -!- SUBUNIT: Heteromultimer with KCNB1 and with KCNB2. Does not form
CC       homomultimers. Might also bind to other channel proteins (By
CC       similarity).
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CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. May not reach the
CC       plasma membrane but remain in an intracellular compartment in the
CC       absence of KCNB1 (By similarity).
CC   -!- TISSUE SPECIFICITY: Detected in lung, spleen, brain and heart.
CC   -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- MISCELLANEOUS: Inhibited by 4-aminopyridine (4-AP). Channel
CC       activity is reversibly inhibited by hypoxia and down-regulated in
CC       the absence of intracellular ATP.
CC   -!- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. S SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF029056; AAB94882.1; -.
DR   EMBL; Y17607; CAA76805.1; -.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR003131; K_tetra.
DR   InterPro; IPR003971; Kv9_channel.
DR   InterPro; IPR003968; Kv_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF02214; K_tetra; 1.
DR   PRINTS; PR00169; KCHANNEL.
DR   PRINTS; PR01494; KV9CHANNEL.
DR   PRINTS; PR01491; KVCHANNEL.
DR   SMART; SM00225; BTB; 1.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Potassium transport; Transmembrane;
KW   Multigene family.
FT   DOMAIN        1    185       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    186    206       SEGMENT S1 (POTENTIAL).
FT   TRANSMEM    224    244       SEGMENT S2 (POTENTIAL).
FT   DOMAIN      245    253       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    254    274       SEGMENT S3 (POTENTIAL).
FT   TRANSMEM    288    308       SEGMENT S4 (POTENTIAL).
FT   DOMAIN      309    323       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    324    344       SEGMENT S5 (POTENTIAL).
FT   DOMAIN      358    378       SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT   TRANSMEM    385    405       SEGMENT S6 (POTENTIAL).
FT   DOMAIN      406    491       CYTOPLASMIC (POTENTIAL).
FT   CONFLICT    113    113       I -> F (IN REF. 1).
SQ   SEQUENCE   491 AA;  55865 MW;  6157BC7EFE94CC2B CRC64;

  Query Match             4.5%;  Score 102;  DB 1;  Length 491;
  Best Local Similarity   25.9%;  Pred. No. 1.7;
  Matches   35;  Conservative   25;  Mismatches   51;  Indels   24;  Gaps    5;
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Qy          20 PNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTA-----NDLAKDSKGRFF 74
               |    |:| |||||       |||:  ||: | |: :   : |     :| :   |  ::
Db          10 PGQDEELVNLNVGGFKQSVDQSTLLRFPHTRLGKLLTCHSEEAILELCDDYSVADK-EYY 68

Qy          75 IDRDGFLFRYILDYLRDRQVVLPDHFPEK---GRLKREAEYFQLPDLVKLLTPDEIKQSP 131
                ||:  ||||:|::    ::    |  |:       :| ||: : :|
Db          69 FDRNPSLFRYVLNFYYTGKL----HVMEELCVFSFCQEIEYWGINELF----------I 113

Qy         132 DEFCHSDFEDASQGS 146
               |  | | :::  : |
Db         114 DSCCSSRYQERKEES 128


RESULT 8
DNM1_CHICK
ID   DNM1_CHICK     STANDARD;      PRT;  1537 AA.
AC   Q92072;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   DNA (cytosine-5)-methyltransferase 1 (EC 2.1.1.37) (Dnmt1) (DNA
DE   methyltransferase GgaI) (DNA MTase GgaI) (MCMT) (M.GgaI).
GN   DNMT1 OR DNMT OR AIM.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96172572; PubMed=8586618;
RA   Tajima S., Tsuda H., Wakabayashi N., Asaso A., Mizuno S.,
RA   Nishimori K.;
RT   "Isolation and expression of a chicken DNA methyltransferase cDNA.";
RL   J. Biochem. 117:1050-1057(1995).
RN   [2]
RP   INTERACTION WITH PCNA, AND MUTAGENESIS OF VAL-190.
RX   MEDLINE=97451025; PubMed=9302295;
RA   Chuang L.S.-H., Ian H.-I., Koh T.-W., Ng H.-H., Xu G., Li B.F.L.;
RT   "Human DNA-(cytosine-5) methyltransferase-PCNA complex as a target for
RT   p21WAF1.";
RL   Science 277:1996-2000(1997).
CC   -!- FUNCTION: Methylates CpG residues. Preferentially methylates
CC       hemimethylated DNA. It is responsible for maintaining methylation
CC       patterns established in development (By similarity). Mediates
CC       transcriptional repression by direct binding to HDAC2 (By
CC       similarity).
CC   -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA = S-adenosyl-L-
CC       homocysteine + DNA containing 5-methylcytosine.
CC   -!- SUBUNIT: Interacts with PCNA.
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC   -!- TISSUE SPECIFICITY: Testis and lung.
CC   -!- SIMILARITY: BELONGS TO THE C5-METHYLTRANSFERASE FAMILY.
CC   -!- SIMILARITY: Contains 2 BAH domains.
CC   -!- SIMILARITY: Contains 1 CXXC-type zinc finger.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; D43920; BAA07867.1; -.
DR   PIR; JC4172; JC4172.
DR   REBASE; 3020; M.GgaI.
DR   InterPro; IPR001025; BAH.
DR   InterPro; IPR001525; C5_DNA_meth.
DR   InterPro; IPR002857; Znf_CXXC.
DR   Pfam; PF01426; BAH; 2.
DR   Pfam; PF00145; DNA_methylase; 1.
DR   Pfam; PF02008; zf-CXXC; 1.
DR   PRINTS; PR00105; C5METTRFRASE.
DR   SMART; SM00439; BAH; 2.
DR   TIGRFAMs; TIGR00675; dcm; 1.
DR   PROSITE; PS00094; C5_MTASE_1; 1.
DR   PROSITE; PS00095; C5_MTASE_2; 1.
KW   Transferase; Methyltransferase; Transcription regulation; Repressor;
KW   DNA-binding; Zinc-finger; Zinc; Metal-binding; Nuclear protein;
KW   Repeat; Phosphorylation.
FT   DOMAIN      182    194       INTERACTS WITH PCNA.
FT   ZN_FING     557    603       CXXC-TYPE.
FT   DOMAIN      667    791       BAH 1.
FT   DOMAIN      877   1011       BAH 2.
FT   DOMAIN     1020   1034       7.5 X 2 AA TANDEM REPEATS OF K-G.
FT   DOMAIN      129    149       POLY-SER.
FT   DOMAIN      217    227       POLY-GLU.
FT   MOD_RES     420    420       PHOSPHORYLATION (BY SIMILARITY).
FT   ACT_SITE   1141   1141       BY SIMILARITY.
FT   MUTAGEN     190    190       V->H: NO LOSS OF INTERACTION WITH PCNA.
SQ   SEQUENCE   1537 AA;  172906 MW;  FB7E0B2CD10EA17E CRC64;

  Query Match             4.4%;  Score 101.5;  DB 1;  Length 1537;
  Best Local Similarity   26.1%;  Pred. No. 8.7;
  Matches   35;  Conservative   19;  Mismatches   63;  Indels   17;  Gaps    2;

Qy        291 CCKNGK-----------GDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNI 339
                  |  ||:           |  | |   : :  |:||  | | :||   :::  |  |:
Db        102 CAGNGEEEWERGGRGEDGAMEVEEAAASSSSSSSSSSSSSSSSSSSSLLPAPRARKARR 161

Qy        340 QTLDRPIKKGPVQLIQQSEMRRKSDLLRILTSGSRESNMSSKKKAVKEKLSI------EE 393
                 :   || |          |:  :| : : || :        ||| ::|       ||
Db        162 SRSNGESKKSPASSRVTRSSGRQPTILSVFSKGSTKRKSEEVNGAVKPEVSAEKDEEEEE 221

Qy        394 ELEKCIQDFLKKKI 407
                |||:  ||  : ||
Db        222 ELEEKEQDEKRIKI 235


RESULT 9
KCS3_HUMAN
ID   KCS3_HUMAN     STANDARD;      PRT;   491 AA.
AC   Q9BQ31; O43651; Q96B56;
```

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Potassium voltage-gated channel subfamily S member 3 (Potassium
DE channel Kv9.3) (Delayed-rectifier K+ channel alpha subunit 3).
GN KCNS3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT THR-450.
RC TISSUE=Lens epithelium;
RX MEDLINE=99413882; PubMed=10484328;
RA Shepard A.R., Rae J.L.;
RT "Electrically silent potassium channel subunits from human lens
RT epithelium.";
RL Am. J. Physiol. 277:C412-C424(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Potassium channel subunit. Modulates channel activity
CC and reduces the ion flow (By similarity).
CC -!- SUBUNIT: Heteromultimer with KCNB1 and with KCNB2. Does not form
CC homomultimers. Might also bind to other channel proteins (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. May not reach the
CC plasma membrane but remain in an intracellular compartment in the
CC absence of KCNB1.
CC -!- TISSUE SPECIFICITY: Detected in most tissues, but not in
CC peripheral blood lymphocytes. The highest levels of expression are
CC in lung.
CC -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -!- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. S SUBFAMILY.

```
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF043472; AAC13164.1; -.
DR   EMBL; BC004148; AAH04148.1; -.
DR   EMBL; BC004987; AAH04987.1; -.
DR   EMBL; BC015947; AAH15947.1; -.
DR   Genew; HGNC:6302; KCNS3.
DR   MIM; 603888; -.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR003131; K_tetra.
DR   InterPro; IPR003971; Kv9_channel.
DR   InterPro; IPR003968; Kv_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF02214; K_tetra; 1.
DR   PRINTS; PR00169; KCHANNEL.
DR   PRINTS; PR01494; KV9CHANNEL.
DR   PRINTS; PR01491; KVCHANNEL.
DR   SMART; SM00225; BTB; 1.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Potassium transport; Transmembrane;
KW   Multigene family; Polymorphism.
FT   DOMAIN        1    185       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    186    206       SEGMENT S1 (POTENTIAL).
FT   TRANSMEM    219    239       SEGMENT S2 (POTENTIAL).
FT   DOMAIN      240    253       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    254    274       SEGMENT S3 (POTENTIAL).
FT   TRANSMEM    288    308       SEGMENT S4 (POTENTIAL).
FT   DOMAIN      309    323       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    324    344       SEGMENT S5 (POTENTIAL).
FT   DOMAIN      358    378       SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT   TRANSMEM    386    406       SEGMENT S6 (POTENTIAL).
FT   DOMAIN      407    491       CYTOPLASMIC (POTENTIAL).
FT   VARIANT     450    450       A -> T.
FT                                /FTId=VAR_014200.
FT   CONFLICT     27     27       S -> Y (IN REF. 2; AAH15947).
FT   CONFLICT    225    225       L -> V (IN REF. 1 AND 2; AAH15947).
SQ   SEQUENCE   491 AA;  55984 MW;  A5F12BF077A50DAD CRC64;

  Query Match             4.4%;  Score 100;  DB 1;  Length 491;
  Best Local Similarity   25.4%;  Pred. No. 2.5;
  Matches   35;  Conservative   28;  Mismatches   61;  Indels   14;  Gaps    5;

Qy         20 PNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTA-----NDLAKDSKGRFF 74
                |    |:| |||||       |||:  ||: | |: :   : |     :| :   |  ::
Db         10 PGQDEELVNLNVGGFKQSVDQSTLLRFPHTRLGKLLTCHSEEAILELCDDYSVADK-EYY 68
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Qy          75 IDRDGFLFRYILDYLRDRQVVLPDHFPEK---GRLKREAEYFQLPDL-VKLLTPDEIKQS 130
               ||:  ||||:|::    ::    |  |:       :| ||: : :| :     :  ::
Db          69 FDRNPSLFRYVLNFYYTGKL----HVMEELCVFSFCQEIEYWGINELFIDSCCSNRYQER 124

Qy         131 PDEFCHSDFEDASQGSDT 148
                :|    |::  |    |
Db         125 KEENHEKDWDQKSHDVST 142


RESULT 10
ADDA_HUMAN
ID   ADDA_HUMAN     STANDARD;      PRT;   737 AA.
AC   P35611; Q13734; Q14729; Q16156; Q9UJB6;
DT   01-JUN-1994 (Rel. 29, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Alpha adducin (Erythrocyte adducin alpha subunit).
GN   ADD1 OR ADDA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., SEQUENCE OF 24-36; 41-47; 516-569 AND 722-729, AND
RP   VARIANT CYS-586.
RC   TISSUE=Reticulocytes;
RX   MEDLINE=92011907; PubMed=1840603;
RA   Joshi R.L., Gilligan D.M., Otto E., McLaughlin T., Bennett V.D.;
RT   "Primary structure and domain organization of human alpha and beta
RT   adducin.";
RL   J. Cell Biol. 115:665-675(1991).
RN   [2]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX   MEDLINE=95293415; PubMed=7774961;
RA   Lin B., Nasir J., McDonald H., Graham R., Rommens J.M., Goldberg Y.P.,
RA   Hayden M.R.;
RT   "Genomic organization of the human alpha-adducin gene and its
RT   alternately spliced isoforms.";
RL   Genomics 25:93-99(1995).
RN   [3]
RP   SEQUENCE OF 121-170 FROM N.A.
RA   Hall C.;
RL   Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 171-737 FROM N.A.
RA   Mungall A.;
RL   Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 531-737 FROM N.A.
RX   MEDLINE=94258208; PubMed=1345173;
RA   Taylor S.A., Snell R.G., Buckler A., Ambrose C., Duyao M.,
RA   Church D., Lin C.S., Altherr M., Bates G.P., Groot N.;
RT   "Cloning of the alpha-adducin gene from the Huntington's disease
RT   candidate region of chromosome 4 by exon amplification.";
RL   Nat. Genet. 2:223-227(1992).
RN   [6]
RP   PHOSPHORYLATION SITES, AND PARTIAL SEQUENCE.
```

```
RX   MEDLINE=96411719; PubMed=8810272;
RA   Matsuoka Y., Hughes C.A., Bennett V.;
RT   "Adducin regulation. Definition of the calmodulin-binding domain and
RT   sites of phosphorylation by protein kinases A and C.";
RL   J. Biol. Chem. 271:25157-25166(1996).
RN   [7]
RP   VARIANT TRP-460.
RX   MEDLINE=98337407; PubMed=9674650;
RA   Kamitani A., Wong Z.Y., Fraser R., Davies D.L., Connor J.M., Foy C.J.,
RA   Watt G.C., Harrap S.B.;
RT   "Human alpha-adducin gene, blood pressure, and sodium metabolism.";
RL   Hypertension 32:138-143(1998).
RN   [8]
RP   VARIANTS TRP-460 AND CYS-586.
RX   MEDLINE=99318094; PubMed=10391210;
RA   Halushka M.K., Fan J.-B., Bentley K., Hsie L., Shen N., Weder A.,
RA   Cooper R., Lipshutz R., Chakravarti A.;
RT   "Patterns of single-nucleotide polymorphisms in candidate genes for
RT   blood-pressure homeostasis.";
RL   Nat. Genet. 22:239-247(1999).
CC   -!- FUNCTION: MEMBRANE-CYTOSKELETON-ASSOCIATED PROTEIN THAT PROMOTES
CC       THE ASSEMBLY OF THE SPECTRIN-ACTIN NETWORK. BINDS TO CALMODULIN.
CC   -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT OR AN ALPHA
CC       AND A GAMMA SUBUNIT.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1;
CC         IsoId=P35611-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P35611-2; Sequence=VSP_000175, VSP_000176;
CC       Name=3;
CC         IsoId=P35611-3; Sequence=VSP_000174;
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES. FOUND IN MUCH HIGHER
CC       LEVELS IN RETICULOCYTES THAN THE BETA SUBUNIT.
CC   -!- DOMAIN: EACH SUBUNIT IS COMPRISED OF THREE REGIONS: A NH2-TERMINAL
CC       PROTEASE-RESISTANT GLOBULAR HEAD REGION, A SHORT CONNECTING
CC       SUBDOMAIN, AND A PROTEASE-SENSITIVE TAIL REGION.
CC   -!- PTM: THE N-TERMINUS IS BLOCKED.
CC   -!- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ADDUCIN
CC       SUBFAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; X58141; CAA41149.1; -.
DR   EMBL; L29296; AAB05645.1; -.
DR   EMBL; L29286; AAB05645.1; JOINED.
DR   EMBL; L29287; AAB05645.1; JOINED.
DR   EMBL; L29289; AAB05645.1; JOINED.
DR   EMBL; L29290; AAB05645.1; JOINED.
DR   EMBL; L29291; AAB05645.1; JOINED.
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DR   EMBL; L29292; AAB05645.1; JOINED.
DR   EMBL; L29293; AAB05645.1; JOINED.
DR   EMBL; L29294; AAB05645.1; JOINED.
DR   EMBL; L29295; AAB05645.1; JOINED.
DR   EMBL; L29297; AAB05645.1; JOINED.
DR   EMBL; L29298; AAB05645.1; JOINED.
DR   EMBL; Z74617; CAA98970.1; -.
DR   EMBL; Z68280; CAA92578.1; -.
DR   EMBL; S70314; AAB30914.2; -.
DR   PIR; S18207; S18207.
DR   Genew; HGNC:243; ADD1.
DR   MIM; 102680; -.
DR   GO; GO:0003779; F:actin binding activity; TAS.
DR   InterPro; IPR001303; Aldolase_II_N.
DR   Pfam; PF00596; Aldolase_II; 1.
KW   Cytoskeleton; Membrane; Calmodulin-binding; Phosphorylation;
KW   Alternative splicing; Polymorphism.
FT   DOMAIN      717    734       CALMODULIN-BINDING (POTENTIAL).
FT   MOD_RES      59     59       PHOSPHORYLATION (BY PKA).
FT   MOD_RES     408    408       PHOSPHORYLATION (BY PKA).
FT   MOD_RES     436    436       PHOSPHORYLATION (BY PKA).
FT   MOD_RES     481    481       PHOSPHORYLATION (BY PKA).
FT   MOD_RES     716    716       PHOSPHORYLATION (BY PKC).
FT   MOD_RES     726    726       PHOSPHORYLATION (BY PKC AND PKA).
FT   VARSPLIC    471    471       K -> KVWTNITHDHVKPLLQSLSSGVCVPSCITNCL (in
FT                                isoform 3).
FT                                /FTId=VSP_000174.
FT   VARSPLIC    621    631       DLVPEPTTGDD -> GDGCAREYLLP (in isoform
FT                                2).
FT                                /FTId=VSP_000175.
FT   VARSPLIC    632    737       Missing (in isoform 2).
FT                                /FTId=VSP_000176.
FT   VARIANT     270    270       Y -> N (in dbSNP:4971).
FT                                /FTId=VAR_014863.
FT   VARIANT     376    376       E -> D (in dbSNP:4972).
FT                                /FTId=VAR_014864.
FT   VARIANT     460    460       G -> W (in dbSNP:4961).
FT                                /FTId=VAR_014184.
FT   VARIANT     510    510       N -> I (in dbSNP:4962).
FT                                /FTId=VAR_014865.
FT   VARIANT     586    586       S -> C (in dbSNP:4963).
FT                                /FTId=VAR_014185.
FT   CONFLICT    606    606       A -> E (IN REF. 2).
SQ   SEQUENCE   737 AA;  80955 MW;  DF13AB30B12F20B6 CRC64;

  Query Match              4.4%;  Score 100;  DB 1;  Length 737;
  Best Local Similarity   18.6%;  Pred. No. 4.3;
  Matches   95;  Conservative   77;  Mismatches  174;  Indels  164;  Gaps   24;

Qy         22 SFPEVVELNVGGQVYFTRHSTLIS--------IPHSLLWKMFSPKRDTANDLAKDSKGRF 73
              :|  : :|    |: :   :| ::        :|  ||:        ||: | | :
Db        151 AFYRLADLFGWSQLIYNHITTRVNSEQEHFLIVPFGLLY-----SEVTASSLVKINLQGD 205

Qy         74 FIDRD---------GFLFRYILDYLR-DRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLT 123
              :||           ||     :   | | : |:  | |  |      :   ||     ::
Db        206 IVDRGSTNLGVNQAGFTLHSAIYAARPDVKCVVHIHTP-AGAAVSAMKCGLLP-----IS 259
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Qy        124 PDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPAD-----RKWGFITVGYRGSCTLGR 178
              |: :  |  |  : |:       : ::    :| |       |  | ::||
Db        260 PEAL--SLGEVAYHDYHGILVDEEEKVLIQKNLGPKSKVLILRNHGLVSVG--------- 308

Qy        179 EGQADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRA----PERYTS---------- 224
                  :  |  :  ::|      | |:   ||  :  ||      ||:| :
Db        309 -ESVEEAFYYIHNLVV------ACEIQVRTLASAGGPDNLVLLNPEKYKAKSRSPGSPVG 361

Qy        225 -------RFYLKFKHLERAFDMLSECGFHM-VACNSSVTASFINQYTDDKIWSSYTEYVF 276
                    :: :  :  |    ||   |:                 :|:| :: :| | | |
Db        362 EGTGSPPKWQIGEQEFEALMRMLDNLGYRTGYPYRYPALREKSKKYSDVEVPASVTGYSF 421

Qy        277 -------------------YREPSRWSPSHCDCCCKNGKGD---KEGESGTSCND----- 309
                              || :||          :|:||   :||::|:|
Db        422 ASDGDSGTCSPLRHSFQKQQREKTRW--------LNSGRGDEASEEGQNGSSPKSKTKWT 473

Qy        310 ------------------LSTSSCDSQS-------------EASSPQETVICGPVTRQTN 338
                             |:|:  : |               : : ||  |:|| |
Db        474 KEDGHRTSTSAVPNLFVPLNTNPKEVQEMRNKIREQNLQDIKTAGPQSQVLCGVV----- 528

Qy        339 IQTLDRPIKKGPVQLIQQSEM---RRKSDLLRILTSG--------SRESNMSSKKKAVKE 387
                 :|| : :|  :|:  |:    :     : : |:|          ||     ::   |:
Db        529 ---MDRSLVQG--ELVTASKAIIEKEYQPHVIVSTTGPNPFTTLTDRELEEYRREVERKQ 583

Qy        388 KLSIEEELEKCIQDFLKKKIPDRFPERKHP 417
              | | || |::  :   |:| |   |   ||
Db        584 KGS-EENLDEAREQ--KEKSPPDQPAVPHP 610
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RESULT 11
KCS3_RABIT
ID   KCS3_RABIT     STANDARD;      PRT;   491 AA.
AC   Q9TT17;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Potassium voltage-gated channel subfamily S member 3 (Potassium
DE   channel Kv9.3) (Delayed-rectifier K+ channel alpha subunit 3).
GN   KCNS3.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=New Zealand white; TISSUE=Corneal epithelium;
RA   Rae J.L.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Potassium channel subunit. Modulates channel activity
CC       and reduces the ion flow (By similarity).
CC   -!- SUBUNIT: Heteromultimer with KCNB1 and with KCNB2. Does not form
CC       homomultimers. Might also bind to other channel proteins (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. May not reach the
CC       plasma membrane but remain in an intracellular compartment in the
CC       absence of KCNB1 (By similarity).
CC   -!- DOMAIN: The segment S4 is probably the voltage-sensor and is
```

```
CC       characterized by a series of positively charged amino acids at
CC       every third position.
CC   -!- SIMILARITY: BELONGS TO THE POTASSIUM CHANNEL FAMILY. S SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF209723; AAF22833.1; -.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR003091; K_channel.
DR   InterPro; IPR003131; K_tetra.
DR   InterPro; IPR003971; Kv9_channel.
DR   InterPro; IPR003968; Kv_channel.
DR   InterPro; IPR005820; M+channel_nlg.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF02214; K_tetra; 1.
DR   PRINTS; PR00169; KCHANNEL.
DR   PRINTS; PR01494; KV9CHANNEL.
DR   PRINTS; PR01491; KVCHANNEL.
DR   SMART; SM00225; BTB; 1.
KW   Transport; Ion transport; Ionic channel; Voltage-gated channel;
KW   Potassium channel; Potassium; Potassium transport; Transmembrane;
KW   Multigene family.
FT   DOMAIN        1    185       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    186    206       SEGMENT S1 (POTENTIAL).
FT   TRANSMEM    224    244       SEGMENT S2 (POTENTIAL).
FT   DOMAIN      245    253       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    254    274       SEGMENT S3 (POTENTIAL).
FT   TRANSMEM    288    308       SEGMENT S4 (POTENTIAL).
FT   DOMAIN      309    323       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    324    344       SEGMENT S5 (POTENTIAL).
FT   DOMAIN      358    378       SEGMENT H5 (PORE-FORMING) (POTENTIAL).
FT   TRANSMEM    386    406       SEGMENT S6 (POTENTIAL).
FT   DOMAIN      407    491       CYTOPLASMIC (POTENTIAL).
SQ   SEQUENCE   491 AA;  55941 MW;  2EE396E0889D6F77 CRC64;

  Query Match             4.3%;  Score 99;  DB 1;  Length 491;
  Best Local Similarity   25.4%;  Pred. No. 3;
  Matches   35;  Conservative   28;  Mismatches   61;  Indels   14;  Gaps    5;

Qy         20 PNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTA-----NDLAKDSKGRFF 74
              |    |:| |||||       |||:  ||: | |: :   : |     :| :   |  ::
Db         10 PGPDEELVNLNVGGFKQSVDQSTLLRFPHTRLGKLLTCHSEEAILELCDDYSVADK-EYY 68

Qy         75 IDRDGFLFRYILDYLRDRQVVLPDHFPEK---GRLKREAEYFQLPDL-VKLLTPDEIKQS 130
               ||:  ||||:|::    ::    |  |:       :| ||: : :| :     :  ::
Db         69 FDRNPSLFRYVLNFYYTGKL----HVMEELCVFSFCQEIEYWGINELFIDSCCSNRYQER 124

Qy        131 PDEFCHSDFEDASQGSDT 148
              :|    |::  |    |
```

```
Db        125 KEENHEKDWDQKSNDVST 142


RESULT 12
IRF1_MOUSE
ID   IRF1_MOUSE     STANDARD;      PRT;   329 AA.
AC   P15314;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Interferon regulatory factor 1 (IRF-1).
GN   IRF1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88311092; PubMed=3409321;
RA   Miyamoto M., Fujita T., Kimura Y., Maruyama M., Harada H.,
RA   Sudo Y., Miyata T., Taniguchi T.;
RT   "Regulated expression of a gene encoding a nuclear factor, IRF-1,
RT   that specifically binds to IFN-beta gene regulatory elements.";
RL   Cell 54:903-913(1988).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 7-111.
RX   MEDLINE=98082978; PubMed=9422515;
RA   Escalante C.R., Yie J., Thanos D., Aggarwal A.K.;
RT   "Structure of IRF-1 with bound DNA reveals determinants of interferon
RT   regulation.";
RL   Nature 391:103-106(1998).
CC   -!- FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION
CC       OF TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON
CC       CONSENSUS SEQUENCE (ICS)) AND ACTIVATES THOSE GENES.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- INDUCTION: By viruses and IFN.
CC   -!- SIMILARITY: Belongs to the IRF family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M21065; AAA39334.1; -.
DR   PIR; A31595; A31595.
DR   PDB; 1IF1; 25-FEB-98.
DR   TRANSFAC; T00422; -.
DR   MGD; MGI:96590; Irf1.
DR   InterPro; IPR001346; IRF.
DR   Pfam; PF00605; IRF; 1.
DR   PRINTS; PR00267; INTFRNREGFCT.
DR   ProDom; PD002355; IRF; 1.
DR   SMART; SM00348; IRF; 1.
DR   PROSITE; PS00601; IRF; 1.
```

```
KW   Transcription regulation; DNA-binding; Activator; Nuclear protein;
KW   Interferon induction; 3D-structure.
FT   DNA_BIND      7    109       TRYPTOPHAN PENTAD REPEAT.
FT   HELIX        12     20
FT   STRAND       33     34
FT   TURN         41     42
FT   TURN         44     45
FT   TURN         48     50
FT   HELIX        54     61
FT   TURN         62     63
FT   HELIX        74     87
FT   STRAND       91     93
FT   STRAND      107    109
SQ   SEQUENCE   329 AA;  37319 MW;  0E5DD23C0D977B34 CRC64;

  Query Match             4.3%;  Score 98;  DB 1;  Length 329;
  Best Local Similarity   20.1%;  Pred. No. 2.1;
  Matches   69;  Conservative   53;  Mismatches  130;  Indels   92;  Gaps   16;

Qy         31 VGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYILDYLR 90
              : | ::  :   :  ||    ||               :|  : |::|  |||   :
Db         21 IPGLIWINKEEMIFQIP----WK-------------HAAKHGWDINKDACLFRSWAIHTG 63

Qy         91 DRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQGSDT-- 148
               :    :  |:  :         |||:      :|:|           :  ::||
Db         64 RYKAGEKEPDPKTWKANFRCAMNSLPDI------EEVKD----------QSRNKGSSAVR 107

Qy        149 --RICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVFG 206
               |: ||  |    ||               |: ::    :   :  :|| :|   : |
Db        108 VYRMLPP--LTRNQRK-------------ERKSKSSRDTKSKTKRKLCGDVS--PDTFS 149

Qy        207 ETLNESRDPDRAPERYTSRFYLKFKHLERAFDM---LSEC-------GFHM--------- 247
              : |: |  ||     ||:: ||  : |:   |:   || |        :||
Db        150 DGLSSSTLPD-DHSSYTTQGYLG-QDLDMERDITPALSPCVVSSSLSEWHMQMDIIPDST 207

Qy        248 -------VACNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 300
                    |:   | : :  ::  : ||     :     | | | |:| |     |||
Db        208 TDLYNLQVSPMPSTSEAATDEDEEGKIAEDLMKLF---EQSEWQPTHID-----GKGYLL 259

Qy        301 GESGTSCNDL-STSSCDSQSEASSPQETVICGPVTRQTNIQTLD 343
               | ||  : :    ||  : |  ||:  :  |     | :: :|
Db        260 NEPGTQLSSVYGDFSCKEEPEIDSPRGDIGIGIQHVFTEMKNMD 303


RESULT 13
SWI3_YEAST
ID   SWI3_YEAST     STANDARD;      PRT;   825 AA.
AC   P32591;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Transcription regulatory protein SWI3 (SWI/SNF complex component SWI3)
DE   (Transcription factor TYE2).
GN   SWI3 OR TYE2 OR YJL176C OR J0495.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
```

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OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92154671; PubMed=1339306;
RA   Peterson C.L., Herskowitz I.;
RT   "Characterization of the yeast SWI1, SWI2, and SWI3 genes, which
RT   encode a global activator of transcription.";
RL   Cell 68:573-583(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Loehning C., Mueller C., Freidel K., Ciriacy M.;
RL   Submitted (NOV-1990) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Obermaier B., Piravandi E., Rinke M., Domdey H.;
RL   Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: INVOLVED IN TRANSCRIPTIONAL ACTIVATION. THE SWI/SNF
CC       COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER
CC       OF GENES. THIS COMPLEX ALTERS CHROMATIN STRUCTURE TO FACILITATE
CC       BINDING OF GENE-SPECIFIC DEDICATED TRANSCRIPTION FACTORS.
CC       INTERACTS WITH THE N-TERMINUS OF SNF2.
CC   -!- SUBUNIT: COMPONENT OF THE SWI/SNF GLOBAL TRANSCRIPTION ACTIVATOR
CC       COMPLEX.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Contains 1 Myb-like domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M84390; AAA35136.1; -.
DR   EMBL; X56792; CAA40112.1; -.
DR   EMBL; Z49451; CAA89470.1; -.
DR   PIR; S26706; S26706.
DR   TRANSFAC; T02400; -.
DR   SGD; S0003712; SWI3.
DR   InterPro; IPR001005; Myb_DNA_binding.
DR   Pfam; PF00249; myb_DNA-binding; 1.
DR   Pfam; PF04433; SWIRM; 1.
DR   SMART; SM00717; SANT; 1.
DR   PROSITE; PS00037; MYB_1; FALSE_NEG.
DR   PROSITE; PS00334; MYB_2; FALSE_NEG.
DR   PROSITE; PS50090; MYB_3; 1.
KW   Transcription regulation; Activator; DNA-binding; Nuclear protein.
FT   DNA_BIND    526    569       MYB.
FT   DOMAIN        1    304       ASP/GLU-RICH (ACIDIC).
FT   DOMAIN      694    722       LEUCINE-ZIPPER.
SQ   SEQUENCE   825 AA;  92926 MW;  DBA2E2022F15F9A6 CRC64;

  Query Match             4.3%;  Score 98;  DB 1;  Length 825;
  Best Local Similarity   24.4%;  Pred. No. 7.1;
  Matches   85;  Conservative   49;  Mismatches  136;  Indels   78;  Gaps   21;
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Qy          95 VLPDHF----PEKGRLKR-EAEYFQLPDLVKLLTPDEIKQSPDEFCHS-DFEDASQGSDT 148
               :: ||     |:|  : | | | |::|   ::: |   |    |  || : :   :
Db         274 IMNDHSKSANPKKTTITRVEPETFEIPQAHEIVIPSYSKWFNLEKIHSIEVQSLPEFFTN 333

Qy         149 RICPPSSLLPADRKW-GFITVGYR------GSCTLGR---EGQADAKFRRVPRILVCGRI 198
               ||  ||       ::  |:   ||       | |  |    | | | ||    :   | |
Db         334 RI--PSKTPEVYMRYRNFMVNSYRLNPNEYFSVTTARRNVSGDAAALFRLHKFLTKWGLI 391

Qy         199 SLAKEVFGETLNESRDPDRAPERYTSRF--------YLKFKHLERAFDMLSECGFHMVAC 250
               :   :|  : | :: :|     :|::|         :  :|   :  ||
Db         392 NY--QVDSKLLPKNIEPP-LTSQYSTRHDAPRGLFPFESYKPSVQLPDM---------- 437

Qy         251 NSSVTASFINQYTDDKIWSSYTEYVFYREPSR------WSPSHCDCCCKNGKGDKEGESG 304
                 :     :|  | |   |  | | : :|  |        ||  |    :  |||    |
Db         438 --AKLKKMMN--TSD---SESTLYKYLKESKRKYDEITHPPSTTD----DENGDKNDNGG 486

Qy         305 TSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQ-SEMRRKS 363
               |::|||             | : |        :|  ||:||  |::::|  |   |
Db         487 KMNNEVSTS-------------TSMTGDANLLEEGET-SRPLKK--VKILEQIDENWSKE 530

Qy         364 DLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRF 411
               || ::|  | :|      | |   |    :  |:||  ||:  | |:|
Db         531 DLQKLL-KGIQEFGADWYKVA---KNVGNKSPEQCILRFLQLPIEDKF 574
```

RESULT 14
FMN_CHICK
ID   FMN_CHICK   STANDARD;   PRT; 1213 AA.
AC   Q05858;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Formin (Limb deformity protein).
GN   LD.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=White leghorn; TISSUE=Embryo;
RX   MEDLINE=92112031; PubMed=1730407;
RA   Trumpp A., Blundell P.A., de la Pompa J.L., Zeller R.;
RT   "The chicken limb deformity gene encodes nuclear proteins expressed
RT   in specific cell types during morphogenesis.";
RL   Genes Dev. 6:14-28(1992).
CC   -!- FUNCTION: IS IMPORTANT FOR MORPHOGENESIS OF LIMB AND KIDNEY AND
CC   MAY BE INVOLVED IN DETERMINING DORSOVENTRAL NEURAL TUBE POLARITY
CC   AND MOTOR NEURON INDUCTION. IT MAY ALSO HAVE A FUNCTION IN
CC   DIFFERENTIATED CELLS OR BE INVOLVED IN MAINTAINING SPECIFIC
CC   DIFFERENTIATED STATES.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=1;
CC   Comment=A number of isoforms are produced;
CC   Name=1;

```
CC         IsoId=Q05858-1; Sequence=Displayed;
CC   -!- TISSUE SPECIFICITY: PRESENT IN THE ADULT BRAIN, KIDNEY, BRAIN,
CC       HEART AND INTESTINE AND THROUGHOUT THE EMBRYO.
CC   -!- DEVELOPMENTAL STAGE: IN THE DEVELOPING LIMB BUD, THE PROTEIN IS
CC       EXPRESSED IN THE APICAL ECTODERMAL RIDGE AND THE MESENCHYMAL
CC       COMPARTMENT, PREDOMINANTLY IN THE POSTERIOR REGION. DURING KIDNEY
CC       MORPHOGENESIS, EXPRESSION IS INITIALLY RESTRICTED TO THE
CC       EPITHELIAL COMPARTMENT OF THE PRONEPHROS AND MESONEPHROS.
CC   -!- SIMILARITY: Contains 1 Formin homology 1 (FH1) domain.
CC   -!- SIMILARITY: Contains 1 Formin homology 2 (FH2) domain.
CC   -!- SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY FAMILY. CAPPUCCINO
CC       SUBFAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X62681; CAA44555.1; -.
DR   PIR; S24286; A41724.
DR   InterPro; IPR003104; FH2.
DR   InterPro; IPR001265; Formin.
DR   Pfam; PF02181; FH2; 1.
DR   PRINTS; PR00828; FORMIN.
DR   SMART; SM00498; FH2; 1.
KW   Nuclear protein; Developmental protein; Coiled coil;
KW   Alternative splicing.
FT   DOMAIN      428    450       COILED COIL (POTENTIAL).
FT   DOMAIN      503    572       COILED COIL (POTENTIAL).
FT   DOMAIN      652    751       FH1 (PRO-RICH).
FT   DOMAIN      766   1171       FH2.
FT   DOMAIN     1050   1125       COILED COIL (POTENTIAL).
SQ   SEQUENCE   1213 AA;  135240 MW;  ADE3EF0B3FB9D862 CRC64;

  Query Match             4.3%;  Score 97.5;  DB 1;  Length 1213;
  Best Local Similarity   21.4%;  Pred. No. 13;
  Matches  104;  Conservative   50;  Mismatches  168;  Indels  165;  Gaps   23;

Qy          4 SGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHS--TLISIPHSL----------L 51
              :  |||  |   | |   | |:|          ||  :  ||: :   |          :
Db          5 NAGCSRQLPERAGPA--ESEPDV----------FTTFAVRTLLGLTTKLESVTPKEEEAV 52

Qy         52 WKMFSPKRDTANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAE 111
               | | |     |  | :   |   | ||
Db         53 LKAFQPLHIDVNTQANNRYER--NDNDGV------------------------------ 79

Qy        112 YFQLPDLVKLLTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYR 171
                      |: :    | | ||  |   ||  |  |     || :    :    |
Db         80 ------------DDSENQHCESCTSDQADPMSGS--RAEPELEPEPAGQN-EILLPHLR 123

Qy        172 GSCTLGREGQADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFK 231
                 |   |   ||       ||| | : :      |:  ||:||| | |  ||:
Db        124 SVQTSLSESDNDA-------ILVQGTL-VHTTSDTESDGESKDPD-ADETGTSK------ 168
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Qy        232 HLERAFDMLSECGFHMVACNSSVTASFINQ----------YTDDKIWSSYTEYVFYREP 280
                        || :  |  |:|     ||           ::|| :    ||   :
Db        169 ----------CGLNNAAL-SAVALDGNNQSKEESDSEGYGHSDDTVGRDDTE--LHPPI 214

Qy        281 SRWSPSHCDCCCKNGKGDKEGESGTSCND-----LSTSSCDSQ---------------- 318
              |:| |   |   ::   |  |:  |  ::     |:|  |  :
Db        215 SQWLPRKLDSILEH---DSSGKDRTLMDEQFSCLLATGECSPELSGEDQRPSADNVSFHK 271

Qy        319 ---SEASSPQETVICGPVTRQTNIQTLD-------RPIKKGPVQLIQQSEMRRKSDLLRI 368
                 :| |        |   |:  : | |       :| ::  : |::  :  :||:
Db        272 AALTERSFQLPAFFSGLRVRKKGLNTEDGETITEIKP-RENDLALLKLRQPVKKSN---- 326

Qy        369 LTSGSRESNMSSKKKA---VKEKLS---------IEEELEKCIQDFLKKKIPDRFPERKH 416
              :|||      ||: ||     |:||          :|  :     | : :  |  || |
Db        327 ITSGLTTKKKSSEPKASPTFLEQLSHLLNIDVSKNDERTQDSGAGFGETEDSDEGPENKA 386

Qy        417 PWQSELL 423
                |:| |
Db        387 SGQTEPL 393
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RESULT 15
PKCB_HUMAN
ID   PKCB_HUMAN     STANDARD;      PRT;  1186 AA.
AC   Q9ULU4; Q13517; Q8WXC5; Q9H1F3; Q9H1F4; Q9H1F5; Q9H1L8; Q9H1L9;
AC   Q9H2G5; Q9NYN3; Q9UIX6;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Protein kinase C binding protein 1 (Rack7) (Cutaneous T-cell lymphoma
DE   associated antigen se14-3) (CTCL tumor antigen se14-3) (Zinc finger
DE   MYND domain containing protein 8).
GN   PRKCBP1 OR RACK7 OR ZMYND8 OR KIAA1125.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Hippocampus;
RX   MEDLINE=20458872; PubMed=11003709;
RA   Fossey S.C., Kuroda S., Price J.A., Pendleton J.K., Freedman B.I.,
RA   Bowden D.W.;
RT   "Identification and characterization of PRKCBP1, a candidate RACK-like
RT   protein.";
RL   Mamm. Genome 11:919-925(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
RC   TISSUE=Testis;
RX   MEDLINE=21143360; PubMed=11149944;
RA   Eichmueller S., Usener D., Dummer R., Stein A., Thiel D.,
RA   Schadendorf D.;
RT   "Serological detection of cutaneous T-cell lymphoma-associated
RT   antigens.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:629-634(2001).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
```

RC   TISSUE=Brain;
RX   MEDLINE=20039618; PubMed=10574461;
RA   Hirosawa M., Nagase T., Ishikawa K.-I., Kikuno R., Nomura N.,
RA   Ohara O.;
RT   "Characterization of cDNA clones selected by the GeneMark analysis
RT   from size-fractionated cDNA libraries from human brain.";
RL   DNA Res. 6:329-336(1999).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21638749; PubMed=11780052;
RA   Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA   Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA   Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA   Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA   Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
RA   Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA   Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
RA   Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
RA   Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA   Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA   Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA   Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA   Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA   Lehvaslaiho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
RA   Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA   Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA   Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA   Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA   Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA   Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA   Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA   Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 6).
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

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RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBUNIT: Interacts in vitro with PRKCB1.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=6;
CC         Comment=Experimental confirmation may be lacking for some
CC         isoforms;
CC       Name=1;
CC         IsoId=Q9ULU4-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q9ULU4-2; Sequence=VSP_000566, VSP_000569;
CC       Name=3;
CC         IsoId=Q9ULU4-3; Sequence=VSP_000564, VSP_000568;
CC       Name=4;
CC         IsoId=Q9ULU4-4; Sequence=VSP_000565, VSP_000568;
CC       Name=5;
CC         IsoId=Q9ULU4-5; Sequence=VSP_000563, VSP_000567;
CC       Name=6;
CC         IsoId=Q9ULU4-6; Sequence=VSP_000564, VSP_000568, VSP_000570;
CC   -!- TISSUE SPECIFICITY: Expressed in all tissues examined with highest
CC       expression in brain, lung, pancreas, and placenta. Expressed in
CC       cutaneous T-cell lymphomas (CTCL).
CC   -!- SIMILARITY: Contains 1 bromodomain.
CC   -!- SIMILARITY: Contains 1 PHD-type zinc finger.
CC   -!- SIMILARITY: Contains 1 PWWP domain.
CC   -!- SIMILARITY: Contains 1 MYND-type zinc finger.
CC   -!- CAUTION: Ref.1 (AAC72244) sequence differs from that shown due to
CC       a frameshift in position 816.
CC   -!- CAUTION: Ref.4 sequence differs from that shown due to erroneous
CC       gene model prediction.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF233453; AAF71262.1; -.
DR   EMBL; U48251; AAC72244.1; ALT_FRAME.
DR   EMBL; AF454056; AAL50790.1; -.
DR   EMBL; AF273045; AAG34905.1; -.
DR   EMBL; AB032951; BAA86439.1; ALT_INIT.
DR   EMBL; AL031666; CAC19780.1; ALT_SEQ.
DR   EMBL; AL031666; CAC19781.1; ALT_TERM.
DR   EMBL; AL031666; CAC19782.1; ALT_TERM.
DR   EMBL; AL390212; CAC15980.2; ALT_INIT.
DR   EMBL; AL390212; CAC15981.1; ALT_SEQ.
DR   EMBL; AL049540; CAB56762.1; -.
DR   EMBL; BC030721; AAH30721.1; -.
DR   Genew; HGNC:9397; PRKCBP1.
DR   InterPro; IPR001487; Bromodomain.
DR   InterPro; IPR000313; PWWP_domain.
DR   InterPro; IPR002893; Znf_MYND.
```

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DR   InterPro; IPR001965; Znf_PHD.
DR   Pfam; PF00439; bromodomain; 1.
DR   Pfam; PF00628; PHD; 1.
DR   Pfam; PF00855; PWWP; 1.
DR   Pfam; PF01753; zf-MYND; 1.
DR   PRINTS; PR00503; BROMODOMAIN.
DR   SMART; SM00297; BROMO; 1.
DR   SMART; SM00249; PHD; 1.
DR   SMART; SM00293; PWWP; 1.
DR   PROSITE; PS50014; BROMODOMAIN_2; 1.
DR   PROSITE; PS50812; PWWP; 1.
DR   PROSITE; PS01360; ZF_MYND_1; 1.
DR   PROSITE; PS50865; ZF_MYND_2; 1.
DR   PROSITE; PS01359; ZF_PHD_1; 1.
DR   PROSITE; PS50016; ZF_PHD_2; 1.
KW   Bromodomain; Zinc-finger; Alternative splicing.
FT   ZN_FING     107    152       PHD-TYPE.
FT   DOMAIN      184    254       BROMODOMAIN.
FT   DOMAIN      296    346       PWWP.
FT   ZN_FING    1028   1062       MYND-TYPE.
FT   DOMAIN     1147   1186       INTERACTS WITH PRKCB1.
FT   DOMAIN       43     47       POLY-LYS.
FT   DOMAIN      838    854       POLY-GLN.
FT   DOMAIN     1089   1092       POLY-SER.
FT   VARSPLIC      1      1       M -> MHPQSLAEEEIKTEQEVVEG (in isoform 5).
FT                                /FTId=VSP_000563.
FT   VARSPLIC      1    145       Missing (in isoform 3 and isoform 6).
FT                                /FTId=VSP_000564.
FT   VARSPLIC      1    376       Missing (in isoform 4).
FT                                /FTId=VSP_000565.
FT   VARSPLIC      1    526       Missing (in isoform 2).
FT                                /FTId=VSP_000566.
FT   VARSPLIC     58     82       Missing (in isoform 5).
FT                                /FTId=VSP_000567.
FT   VARSPLIC    823    869       SKFQTSSQKWHMQKMQRQQQQQQQQNQQQQPQSSQGTRYQT
FT                                RQAVKA -> T (in isoform 3, isoform 4 and
FT                                isoform 6).
FT                                /FTId=VSP_000568.
FT   VARSPLIC    824    869       Missing (in isoform 2).
FT                                /FTId=VSP_000569.
FT   VARSPLIC   1142   1142       D -> VSKRCDKQPAYAPTTTDHQPHPNYPAQKY (in
FT                                isoform 6).
FT                                /FTId=VSP_000570.
FT   CONFLICT    391    391       I -> V (IN REF. 2; AAL50790).
FT   CONFLICT    894    894       P -> A (IN REF. 2).
SQ   SEQUENCE   1186 AA;  131692 MW;  BAE8CDEF240E647A CRC64;

  Query Match             4.2%;  Score 96.5;  DB 1;  Length 1186;
  Best Local Similarity   18.9%;  Pred. No. 15;
  Matches   66;  Conservative   51;  Mismatches  114;  Indels  119;  Gaps   16;

Qy        133 EFCHSDFEDASQGSDTRICPPSSLLPADRKW----GFITVGYRGSCTLGREGQADAKF-- 186
              | |   :  | |  |   | | |  |    |    ||    :       ::|| ||:|
Db        253 EVCPECYLAACQKRDNWFCEPCS-NPHPLVWAKLKGF--PFWPAKALRDKDGQVDARFFG 309

Qy        187 ----------------RRVPRILVCGRISLAKEVFGETLNE---------------SRDP 215
                             : :|       :   | :|   : |               :  |
```

```
Db        310 QHDRAWVPINNCYLMSKEIP-----FSVKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSP 364

Qy        216 DRAPERYTSRFYL---------------KFKHLERAFDM---------------------- 239
               | |    |:: :                | : ::  |||
Db        365 FRTPYTPNSQYQMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKILMSKPVLSGGTGRRI 424

Qy        240 -LSECGFHMVACNSSV-TASFINQYTDDKIWSSY----TEYVFYREPSRWSPSHCDCCCK 293
               ||:     :: |||| | | : |  : |  ||:     | : : : |  ||:
Db        425 SLSDMPRSPMSTNSSVHTGSDVEQDAEKKATSSHFSASEESMDFLDKSTASPA------- 477

Qy        294 NGKGDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQL 353
                 | |::|         |     :  |||   :  |:| :|     |:    | :
Db        478 ---STKTGQAG---------SLSGSPKPFSPQ---LSAPITTKT-----DKTSTTGSILN 517

Qy        354 IQQSEMRRKSDLLRILTSGSRESN---MSSKKKAVKEK--LSIEEELEKC 398
              :     : : ||  :  |  ::|    : | |: :: :  |:::: :| |
Db        518 LNLDRSKAEMDLKELSESVQQQSTPVPLISPKRQIRSRFQLNLDKTIESC 567
```

Search completed: January 29, 2004, 02:54:05
Job time : 24 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: January 29, 2004, 02:30:11 ; Search time 64 Seconds
(without alignments)
1725.727 Million cell updates/sec

Title: US-10-056-884A-2
Perfect score: 2284
Sequence: 1 MALSGNCSRYYPREQGSAVP.....DRFPERKHPWQSELLRKYHL 428

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

1	2271	99.4	435	4	Q9P2M9	Q9p2m9 homo sapien
2	1278.5	56.0	476	11	Q8C906	Q8c906 mus musculu
3	1272	55.7	477	11	Q8C9B0	Q8c9b0 mus musculu
4	1260.5	55.2	476	11	Q8BR74	Q8br74 mus musculu
5	1125.5	49.3	438	11	Q8CAA9	Q8caa9 mus musculu
6	921.5	40.3	346	11	Q8C4C2	Q8c4c2 mus musculu
7	888.5	38.9	292	11	Q8C7J6	Q8c7j6 mus musculu
8	832	36.4	325	4	Q96CX2	Q96cx2 homo sapien
9	538.5	23.6	228	5	Q9VDH3	Q9vdh3 drosophila
10	537	23.5	111	11	Q9CQU2	Q9cqu2 mus musculu
11	389.5	17.1	156	11	Q8CBQ4	Q8cbq4 mus musculu
12	208.5	9.1	283	11	Q8K0E1	Q8k0e1 mus musculu
13	204	8.9	216	4	Q8N3Q9	Q8n3q9 homo sapien
14	204	8.9	229	4	Q8IU75	Q8iu75 homo sapien
15	204	8.9	272	4	Q8N5I3	Q8n5i3 homo sapien
16	202.5	8.9	228	4	Q8TCA6	Q8tca6 homo sapien
17	202.5	8.9	237	4	Q8NBS6	Q8nbs6 homo sapien
18	201.5	8.8	237	11	Q8BNL5	Q8bnl5 mus musculu
19	201.5	8.8	283	4	Q96SI1	Q96si1 homo sapien
20	196	8.6	191	11	Q8C6V1	Q8c6v1 mus musculu
21	194	8.5	259	11	Q9CYK4	Q9cyk4 mus musculu
22	193.5	8.5	237	4	Q8NC69	Q8nc69 homo sapien
23	192	8.4	259	11	Q9D7X1	Q9d7x1 mus musculu
24	192	8.4	259	11	Q8CCQ3	Q8ccq3 mus musculu
25	189	8.3	225	4	Q9BQ13	Q9bq13 homo sapien
26	189	8.3	259	4	Q8WVF5	Q8wvf5 homo sapien
27	187	8.2	333	4	Q8WUN2	Q8wun2 homo sapien
28	169.5	7.4	207	5	O16612	O16612 caenorhabdi
29	168.5	7.4	234	4	Q9BVI6	Q9bvi6 homo sapien
30	167.5	7.3	338	5	Q9W2F9	Q9w2f9 drosophila
31	166	7.3	234	4	Q96N73	Q96n73 homo sapien
32	165	7.2	222	11	Q8C004	Q8c004 mus musculu
33	165	7.2	234	11	Q8R3T6	Q8r3t6 mus musculu
34	163.5	7.2	288	4	Q8IVR0	Q8ivr0 homo sapien
35	163.5	7.2	289	4	Q96MP8	Q96mp8 homo sapien
36	163	7.1	234	4	Q9NXV2	Q9nxv2 homo sapien
37	161.5	7.1	239	11	Q8C0S7	Q8c0s7 mus musculu
38	161.5	7.1	289	11	Q8BJK1	Q8bjk1 mus musculu
39	159	7.0	234	11	Q8VC57	Q8vc57 mus musculu
40	158.5	6.9	272	5	Q18776	Q18776 caenorhabdi
41	158	6.9	670	5	O17001	O17001 caenorhabdi
42	157.5	6.9	211	5	Q9W579	Q9w579 drosophila
43	157.5	6.9	308	5	O76889	O76889 drosophila
44	156	6.8	220	5	Q18986	Q18986 caenorhabdi
45	153	6.7	298	10	Q9SE95	Q9se95 arabidopsis

ALIGNMENTS

RESULT 1
Q9P2M9
ID Q9P2M9 PRELIMINARY; PRT; 435 AA.
AC Q9P2M9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

```
DE   Hypothetical protein KIAA1317 (Fragment).
GN   KIAA1317.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20181126; PubMed=10718198;
RA   Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes.XVI.
RT   The complete sequences of 150 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 7:65-73(2000).
DR   EMBL; AB037738; BAA92555.1; -.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR003131; K_tetra.
DR   Pfam; PF02214; K_tetra; 1.
DR   SMART; SM00225; BTB; 1.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   435 AA;  49936 MW;  5437FD0FED211B6B CRC64;

  Query Match             99.4%;  Score 2271;  DB 4;  Length 435;
  Best Local Similarity   99.5%;  Pred. No. 5e-198;
  Matches  426;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 67

Qy         61 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVK 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVK 127

Qy        121 LLTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 LLTPDEIKQSPDEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREG 187

Qy        181 QADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFKHLERAFDML 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 QADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYLKFKHLERAFDML 247

Qy        241 SECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 SECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPSHCDCCCKNGKGDKE 307

Qy        301 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEMR 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 GESGTSCNDLSTSSCDSQSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEMR 367

Qy        361 RKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQS 420
              ||||||| |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        368 RKSDLLRTLTSGSRESNMSSKKKAVKEKLSIEEELEKCIQDFLKIKIPDRFPERKHPWQS 427

Qy        421 ELLRKYHL 428
```

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                ||||||||
Db        428 ELLRKYHL 435


RESULT 2
Q8C906
ID   Q8C906      PRELIMINARY;      PRT;   476 AA.
AC   Q8C906;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK043351; BAC31527.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   476 AA;  52782 MW;  219BEC5D104A53DF CRC64;

  Query Match             56.0%;  Score 1278.5;  DB 11;  Length 476;
  Best Local Similarity   59.8%;  Pred. No. 1.1e-107;
  Matches  268;  Conservative   45;  Mismatches   94;  Indels   41;  Gaps    9;

Qy         16 GSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTA-----NDLAKDSK 70
              |   |: |||||||||||||| |:||||:|:| | |  ||||           || :||:
Db         35 GPCAPSPFPEVVELNVGGQVYVTKHSTLLSVPDSTLASMFSPSSPRGGARRRGDLPRDSR 94

Qy         71 GRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQS 130
              ||||||||||||:||||||:|: ||:||||| || ||||:||| ||||||:|   ||:
Db         95 ARFFIDRDGFLFRYVLDYLRDKQLALPEHFPEKERLLREAEFFQLTDLVKLLSPKVTKQN 154

Qy        131 P--DEFCHSDFED-ASQGSDTRICPPSSLLPA-------------------DRKWGFITV 168
                 || | || ||  ||||   :    :   |                   |:: ||:|:
Db        155 SLNDECCQSDLEDNVSQGSSDALLLRGAAAGAPSGSGAHGVSGVVGGGSAPDKRSGFLTL 214

Qy        169 GYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYL 228
              ||||| |  |: ||||||||| ||:|||||:|||||||:|||||||||| ||:||||||
Db        215 GYRGSYTTVRDNQADAKFRRVARIMVCGRIALAKEVFGDTLNESRDPDRQPEKYTSRFYL 274

Qy        229 KFKHLERAFDMLSECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSR-WSPSH 287
              || :||:||| ||| |||||||||| ||:|:||| ||||||||||:|:| | :  ||
Db        275 KFTYLEQAFDRLSEAGFHMVACNSSGTAAFVNQYRDDKIWSSYTEYIFFRPPQKIVSPKQ 334

Qy        288 CDCCCKNGK-GDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGP------VTRQTNIQ 340
                   |  |  ||  |||||||:|||||||| ||||:||:     |          | |
Db        335 EHEDRKRDKVTDKGSESGTSCNELSTSSCDSHSEASTPQD----NPANTQQAAAHQPNTL 390
```

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Qy        341 TLDRPIKKGPVQLIQQSEMRRKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQ 400
              ||||| :| ||| :   : ||||:| : | | |||:|:| ||  | ||||:|||::||||
Db        391 TLDRPSRKAPVQWMPPPDKRRKSELFQSLISKSRETNLSKKK--VCEKLSVEEEMKKCIQ 448

Qy        401 DFLKKKIPDRFPERKHPWQSELLRKYHL 428
              || |  ||| |||||  ||||||:|| |
Db        449 DFKKIHIPDCFPERKRQWQSELLQKYGL 476


RESULT 3
Q8C9B0
ID   Q8C9B0      PRELIMINARY;      PRT;   477 AA.
AC   Q8C9B0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK042569; BAC31296.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   477 AA;  52978 MW;  EB44F32A68E9AEA4 CRC64;

  Query Match             55.7%;  Score 1272;  DB 11;  Length 477;
  Best Local Similarity   59.7%;  Pred. No. 4.4e-107;
  Matches  268;  Conservative   46;  Mismatches   93;  Indels   42;  Gaps   10;

Qy         16 GSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPK--RDTA----NDLAKDS 69
              |   |: |||:|||||||||| |:||||:|:| | |  ||||   |  |     || :||
Db         35 GPCAPSPFPEIVELNVGGQVYVTKHSTLLSVPDSTLASMFSPSSPRGRAPRRRGDLPRDS 94

Qy         70 KGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQ 129
              : ||||||||||||:||||||:|: ||:||||| || ||||:||| ||||||:|   ||
Db         95 RARFFIDRDGFLFRYVLDYLRDKQLALPEHFPEKERLLREAEFFQLTDLVKLLSPKVTKQ 154

Qy        130 SP--DEFCHSDFED-ASQGSDTRICPPSSLLPA-------------------DRKWGFIT 167
              :   || | || ||  ||||   :    :   |                   |:: ||:|
Db        155 NSLNDECCQSDLEDNVSQGSSDALLLRGAAAGAPSGSGAHGVSGVVGGGSAPDKRSGFLT 214

Qy        168 VGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFY 227
              :||||| |  |: ||||||||| ||:|||||:|||||||:|||||||||| ||:||||||
Db        215 LGYRGSYTTVRDNQADAKFRRVARIMVCGRIALAKEVFGDTLNESRDPDRQPEKYTSRFY 274

Qy        228 LKFKHLERAFDMLSECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSR-WSPS 286
              ||| :||:||| ||| ||||||||||| ||:|:||| ||||||||||:|:| | :  ||
Db        275 LKFTYLEQAFDRLSEAGFHMVACNSSGTAAFVNQYRDDKIWSSYTEYIFFRPPQKIVSPK 334
```

```
Qy        287 HCDCCCKNGK-GDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGP------VTRQTNI 339
                    |  |  ||  |||||||:|||||||| ||||:||:     |          | |
Db        335 QEHEDRKRDKVTDKGSESGTSCNELSTSSCDSHSEASTPQD----NPANTQQAAAHQPNT 390

Qy        340 QTLDRPIKKGPVQLIQQSEMRRKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCI 399
               ||||| :| ||| :   : || |:| : | | |||:|:| ||  | ||||:|||::|||
Db        391 LTLDRPSRKAPVQWMPPPDKRRNSELFQSLISKSRETNLSKKK--VCEKLSVEEEMKKCI 448

Qy        400 QDFLKKKIPDRFPERKHPWQSELLRKYHL 428
              ||| |  ||| |||||  ||||||:|| |
Db        449 QDFKKIHIPDCFPERKRQWQSELLQKYGL 477


RESULT 4
Q8BR74
ID   Q8BR74      PRELIMINARY;      PRT;   476 AA.
AC   Q8BR74;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK045439; BAC32368.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   476 AA;  52892 MW;  381C955B9A3DE3F1 CRC64;

  Query Match             55.2%;  Score 1260.5;  DB 11;  Length 476;
  Best Local Similarity   59.2%;  Pred. No. 4.9e-106;
  Matches  265;  Conservative   45;  Mismatches   97;  Indels   41;  Gaps    9;

Qy         16 GSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTA-----NDLAKDSK 70
              |   |: |||||||||||||| |:||||:|:| | |  ||||           || :||:
Db         35 GPCAPSPFPEVVELNVGGQVYVTKHSTLLSVPDSTLASMFSPSSPRGGARRRGDLPRDSR 94

Qy         71 GRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQS 130
               ||||||||||||:||||||:|: ||:||||| || ||||:||| ||||||:|   ||:
Db         95 ARFFIDRDGFLFRYVLDYLRDKQLALPEHFPEKERLLREAEFFQLTDLVKLLSPKVTKQN 154

Qy        131 P--DEFCHSDFED-ASQGSDTRICPPSSLLPAD------------------RKWGFITV 168
                 || | || ||  ||||   :    :   |                   :: ||:|:
Db        155 SLNDECCQSDLEDNVSQGSSDALLLRGAAAGAPSGSGAHGVSGVVGGGSAPYKRSGFLTL 214

Qy        169 GYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYL 228
              |||||  |  |: ||||||||| ||:||||||:|||||||:|||||||||| ||:|||||||
```

```
Db        215 GYRGSYTTVRDNQADAKFRRVARIMVCGRIALAKEVFGDTLNESRDPDRQPEKYTSRFYL 274

Qy        229 KFKHLERAFDMLSECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSR-WSPSH 287
              || :||:||| ||| |||||||||| ||:|:||| ||||||||||:|:| | :  ||
Db        275 KFTYLEQAFDRLSEAGFHMVACNSSGTAAFVNQYRDDKIWSSYTEYIFFRPPQKIVSPKQ 334

Qy        288 CDCCCKNGK-GDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGP------VTRQTNIQ 340
                   |  |  ||  |||||||:| |||||| ||||:||:     |         | |
Db        335 EHEDRKRDKVTDKGSESGTSCNELYTSSCDSHSEASTPQD----NPANTQQAAAHQPNTL 390

Qy        341 TLDRPIKKGPVQLIQQSEMRRKSDLLRILTSGSRESNMSSKKKAVKEKLSIEEELEKCIQ 400
              ||||| :| ||| :   : || |:| : | | |||:|:| ||  | ||||:|||::||||
Db        391 TLDRPSRKAPVQWMPPPDKRRNSELFQSLISKSRETNLSKKK--VCEKLSVEEEMKKCIQ 448

Qy        401 DFLKKKIPDRFPERKHPWQSELLRKYHL 428
              || |  ||| |||||  ||||||:|| |
Db        449 DFKKIHIPDCFPERKRQWQSELLQKYGL 476
```

RESULT 5
Q8CAA9
ID   Q8CAA9   PRELIMINARY;   PRT;   438 AA.
AC   Q8CAA9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK039167; BAC30262.1; -.
KW   Hypothetical protein.
FT   NON_TER   438   438
SQ   SEQUENCE   438 AA; 48062 MW; 7499764AE3745B1D CRC64;

  Query Match   49.3%; Score 1125.5; DB 11; Length 438;
  Best Local Similarity   58.3%; Pred. No. 8.4e-94;
  Matches 239; Conservative   42; Mismatches   88; Indels   41; Gaps   9;

```
Qy         16 GSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTA-----NDLAKDSK 70
              |   |: |||||||||||||| |:||||:|:| | |  ||||           || :||:
Db         35 GPCAPSPFPEVVELNVGGQVYVTKHSTLLSVPDSTLASMFSPSSPRGGARRRGDLPRDSR 94

Qy         71 GRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQS 130
               ||||||||||||:||||||:|: ||:||||| || ||||:||| ||||||:|   ||:
Db         95 ARFFIDRDGFLFRYVLDYLRDKQLALPEHFPEKERLLREAEFFQLTDLVKLLSPKVTKQN 154
```

```
Qy        131 P--DEFCHSDFED-ASQGSDTRICPPSSLLPA------------------DRKWGFITV 168
                 |: | || ||  ||||   :    :   |                    |:: ||:|:
Db        155 SLNDKCCQSDLEDNVSQGSSDALLLRGAAAGAPSGSGAHGVSGVVGGGSAPDKRSGFLTL 214

Qy        169 GYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYL 228
              ||||| |  |: ||||||||| ||:|||||:|||||||:|||||||||| ||:|||||||
Db        215 GYRGSYTTVRDNQADAKFRRVARIMVCGRIALAKEVFGDTLNESRDPDRQPEKYTSRFYL 274

Qy        229 KFKHLERAFDMLSECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYREPSR-WSPSH 287
              || :||:||| ||| |||||||||| ||:|:||| |||||||||||:|:| | :  ||
Db        275 KFTYLEQAFDRLSEAGFHMVACNSSGTAAFVNQYRDDKIWSSYTEYIFFRPPQKIVSPKQ 334

Qy        288 CDCCCKNGK-GDKEGESGTSCNDLSTSSCDSQSEASSPQETVICGP------VTRQTNIQ 340
                   |  |  ||  |||||||:|||||||| ||||:||:     |         | |
Db        335 EHEDRKRDKVTDKGSESGTSCNELSTSSCDSHSEASTPQD----NPANTQQAAAHQPNTL 390

Qy        341 TLDRPIKKGPVQLIQQSEMRRKSDLLRILTSGSRESNMSSKKKAVKEKLS 390
              ||||| :| ||| :   : || |:| : | | |||:|:| ||  | ||||
Db        391 TLDRPSRKAPVQWMPPPDKRRNSELFQSLISKSRETNLSKKK--VCEKLS 438
```

RESULT 6
Q8C4C2
ID Q8C4C2 PRELIMINARY; PRT; 346 AA.
AC Q8C4C2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK082563; BAC38532.1; -.
KW Hypothetical protein.
SQ SEQUENCE 346 AA; 37981 MW; 0A52BB7F33D59D37 CRC64;

  Query Match 40.3%; Score 921.5; DB 11; Length 346;
  Best Local Similarity 62.5%; Pred. No. 2.2e-75;
  Matches 182; Conservative 32; Mismatches 50; Indels 27; Gaps 4;

```
Qy         16 GSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTA-----NDLAKDSK 70
              |   |: |||||||||||||| |:||||:|:| | |  ||||           || :||:
Db         35 GPCAPSPFPEVVELNVGGQVYVTKHSTLLSVPDSTLASMFSPSSPRGGARRRGDLPRDSR 94

Qy         71 GRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQS 130
              |||||||||||||:||||||:|: ||:||||| || ||||:||| ||||||:|:  ||:
Db         95 ARFFIDRDGFLFRYVLDYLRDKQLALPEHFPEKERLLREAEFFQLTDLVKLLSPEVTKQN 154
```

```
Qy        131 P--DEFCHSDFED-ASQGSDTRICPPSSLLPA-------------------DRKWGFITV 168
                 || | || ||  ||||   :    :   |                    |:: ||:|:
Db        155 SLNDECCQSDLEDNVSQGSSDALLLRGAAAGAPSGSGAHGVSGVVGGGSAPDKRSGFLTL 214

Qy        169 GYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDRAPERYTSRFYL 228
              ||||| |  |: ||||||||| ||:|||||:|||||||:|||||||||| ||:|||||||
Db        215 GYRGSYTTVRDNQADAKFRRVARIMVCGRIALAKEVFGDTLNESRDPDRQPEKYTSRFYL 274

Qy        229 KFKHLERAFDMLSECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFYRE 279
              || :||:||| ||| |||||||||| ||:|:||| ||||||||||:|:|:
Db        275 KFTYLEQAFDRLSEAGFHMVACNSSGTAAFVNQYRDDKIWSSYTEYIFFRK 325


RESULT 7
Q8C7J6
ID   Q8C7J6      PRELIMINARY;      PRT;   292 AA.
AC   Q8C7J6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical K+ channel tetramerisation domain containing
DE   protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK050097; BAC34065.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   292 AA;  33285 MW;  4986B75B7C054D44 CRC64;

  Query Match             38.9%;  Score 888.5;  DB 11;  Length 292;
  Best Local Similarity   59.3%;  Pred. No. 1.8e-72;
  Matches  179;  Conservative   35;  Mismatches   55;  Indels   33;  Gaps    5;

Qy          1 MALSGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRD 60
              ||:    |   | |:      ||||::||||||||| ||: |||||| | ||:||| |
Db          1 MAMPEKSSDVKPTEE----CGSFPEIIELNVGGQVYITRYPTLISIPGSRLWEMFSVKNP 56

Qy         61 TANDLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVK 120
               :  | :|:|||||||||||||||:|||:|| |||||||||| ||| ||||||:||:| |
Db         57 CS--LIQDNKGRFFIDRDGFLFRYVLDYMRDMQVVLPDHFPECGRLHREAEYFKLPELAK 114

Qy        121 LLTP--DEIKQSPDEFCHSDFEDASQGSDT---------------------RICPPSSLL 157
              :| |  :::    :: |  | |: |   ||                     |  | | |
Db        115 MLAPKMNKLNSIGNDSCPIDLEELSPSIDTTFNFSSTNSIHISGPDNPMVLRAAPGSEL- 173

Qy        158 PADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVFGETLNESRDPDR 217
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              :| ||||:|||||  ||||: |||||||||  ||:|||:||||||||:||||||||||
Db        174 ---KKAGFITIGYRGSYTLGRDSQADAKFRRVARIMVCGKISLAKEVFGDTLNESRDPDR 230

Qy        218 APERYTSRFYLKFKHLERAFDMLSECGFHMVACNSSVTASFINQYTDDKIWSSYTEYVFY 277
              |||||||:||||  ||:||| |:: |||||||||: | :  :  |||:||:||||||||
Db        231 PPERYTSRYYLKFTFLEQAFDKLADAGFHMVACNSTGTCTVTHDQTDDRIWTSYTEYVFY 290

Qy        278 RE 279
              ||
Db        291 RE 292


RESULT 8
Q96CX2
ID   Q96CX2      PRELIMINARY;      PRT;   325 AA.
AC   Q96CX2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis, and Embryonic carcinoma;
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC013764; AAH13764.1; -.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR003131; K_tetra.
DR   Pfam; PF02214; K_tetra; 1.
DR   SMART; SM00225; BTB; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   325 AA;  35700 MW;  6254CC18E27275A9 CRC64;

  Query Match             36.4%;  Score 832;  DB 4;  Length 325;
  Best Local Similarity   54.0%;  Pred. No. 2.8e-67;
  Matches  170;  Conservative   41;  Mismatches   56;  Indels   48;  Gaps    6;

Qy          4 SGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTAN 63
              ||: |        || |  ||::||||||||| ||  |::|:| ||||:||: ::
Db         20 SGSSS-------SSAEPPLFPDIVELNVGGQVYVTRRCTVVSVPDSLLWRMFTQQQ--PQ 70

Qy         64 DLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLL- 122
              :||:|||||||:|||||||||||||| |:||||:|||: ||:||||||:||:||: |
Db         71 ELARDSKGRFFLDRDGFLFRYILDYLRDLQLVLPDYFPERSRLQREAEYFELPELVRRLG 130

Qy        123 TPDEIKQSP--------------DEFCHSDFEDASQ----------------------GS 146
               | :    |              ||     : :  |                      |:
Db        131 APQQPGPGPPPSRRGVHKEGSLGDELLPLGYSEPEQQEGASAGAPSPTLELASRSPSGGA 190

Qy        147 DTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKEVFG 206
                :  ||  |   |: |:||:||||| |:||: ||||||||| || |||: ||||||||
Db        191 AGPLLTPSQSLDGSRRSGYITIGYRGSYTIGRDAQADAKFRRVARITVCGKTSLAKEVFG 250
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Qy        207 ETLNESRDPDRAPERYTSRFYLKFKHLERAFDMLSECGFHMVACNSSVTASFIN--QYTD 264
              :|||||||||| |||||||:||||  ||:||| ||| |||||||:|: | :| :    ::
Db        251 DTLNESRDPDRPPERYTSRYYLKFNFLEQAFDKLSESGFHMVACSSTGTCAFASSTDQSE 310

Qy        265 DKIWSSYTEYVFYRE 279
              ||||:||||||| ||
Db        311 DKIWTSYTEYVFCRE 325


RESULT 9
Q9VDH3
ID   Q9VDH3      PRELIMINARY;      PRT;   228 AA.
AC   Q9VDH3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CG10830 protein (GH08630P).
GN   CG10830.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
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RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA   Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA   Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
RA   Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003732; AAF55820.1; -.
DR   EMBL; AY060259; AAL25298.1; -.
DR   FlyBase; FBgn0038839; CG10830.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR003131; K_tetra.
DR   Pfam; PF02214; K_tetra; 1.
DR   SMART; SM00225; BTB; 1.
SQ   SEQUENCE   228 AA;  25970 MW;  001CB30B990EB6A1 CRC64;

  Query Match             23.6%;  Score 538.5;  DB 5;  Length 228;
  Best Local Similarity   44.3%;  Pred. No. 9e-41;
  Matches  116;  Conservative   44;  Mismatches   61;  Indels   41;  Gaps    7;

Qy         24 PEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFLFR 83
              ||::||||||  | |  :||:    :|| ::|   ||:   ||||||||:|:|||| |||
Db          2 PEIIELNVGGVSYTTTLATLLQDKSTLLAELFGEGRDS---LAKDSKGRYFLDRDGVLFR 58

Qy         84 YILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSPDEFCHSDFEDAS 143
              ||||:|||: : ||: | |: || ||||:|:|  ::: :  :
Db         59 YILDFLRDKALHLPEGFRERQRLLREAEHFKLTAMLECIRSER----------------- 101

Qy        144 QGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPRILVCGRISLAKE 203
                 | |  ||          | ||:|||||   |::| || |||:: |||||||::  :|
Db        102 ---DAR--PP----------GCITIGYRGSFQFGKDGLADVKFRKLSRILVCGRVAQCRE 146

Qy        204 VFGETLNESRDPDR-APERYTSRFYLKFKHLERAFDMLSECGFHMV-ACNSSVTASFINQ 261
              |||:|||||||||    :||||||:||  ::|:||| | : |: |  :| |    |
Db        147 VFGDTLNESRDPDHGGTDRYTSRFFLKHCYIEQAFDNLHDHGYRMAGSCGSGTAGSAAEP 206

Qy        262 Y----TDDKIWSSYTEYVFYRE 279
                   |::  |: | |:|| |:
Db        207 KPGVDTEENRWNHYNEFVFIRD 228


RESULT 10
Q9CQU2
ID   Q9CQU2      PRELIMINARY;      PRT;   111 AA.
AC   Q9CQU2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   4930434H12Rik protein (Fragment).
GN   4930434H12RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Testis;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK006368; BAB24550.1; -.
DR   EMBL; AK005863; BAB24283.1; -.
DR   MGD; MGI:1914659; 4930434H12Rik.
FT   NON_TER       1      1
SQ   SEQUENCE   111 AA;  12871 MW;  59C93665761F390C CRC64;

  Query Match             23.5%;  Score 537;  DB 11;  Length 111;
  Best Local Similarity   94.6%;  Pred. No. 4.7e-41;
  Matches  105;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        318 QSEASSPQETVICGPVTRQTNIQTLDRPIKKGPVQLIQQSEMRRKSDLLRILTSGSRESN 377
              :||||||||||||||||:||||||||||||||||||||||||| |||||||||
Db          1 ESEASSPQETVICGPVTRQSNIQTLDRPIKKGPVQLIQQSEMRRKSDLLRTLTSGSRESN 60

Qy        378 MSSKKKAVKEKLSIEEELEKCIQDFLKKKIPDRFPERKHPWQSELLRKYHL 428
              :|||||| |||||||||||||||||| |||||||||||||||||||||||
Db         61 ISSKKKAAKEKLSIEEELEKCIQDFLKIKIPDRFPERKHPWQSELLRKYHL 111


RESULT 11
Q8CBQ4
ID   Q8CBQ4      PRELIMINARY;      PRT;   156 AA.
AC   Q8CBQ4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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DE   Inferred: KIAA1317 protein.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK035535; BAC29094.1; -.
SQ   SEQUENCE   156 AA;  17139 MW;  7A94B22AD58D2A3A CRC64;

  Query Match             17.1%;  Score 389.5;  DB 11;  Length 156;
  Best Local Similarity   63.0%;  Pred. No. 2e-27;
  Matches   75;  Conservative   20;  Mismatches   15;  Indels    9;  Gaps    2;

Qy          4 SGNCSRYYPREQGSAVPNSFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTAN 63
              ||: |        || |  ||::||||||||| ||  |::|:| ||||:||: ::
Db         20 SGSSS-------SSAEPPLFPDIVELNVGGQVYVTRRCTVVSVPDSLLWRMFTQQQ--PQ 70

Qy         64 DLAKDSKGRFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLL 122
              :||:|||||||:|||||||||||||||| |:||||:|||: ||:||||||:||:||: |
Db         71 ELARDSKGRFFLDRDGFLFRYILDYLRDLQLVLPDYFPERSRLQREAEYFELPELVRRL 129


RESULT 12
Q8K0E1
ID   Q8K0E1      PRELIMINARY;      PRT;   283 AA.
AC   Q8K0E1;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein (Hypothetical BTB/POZ domain containing
DE   protein).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
```

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DR   EMBL; BC031749; AAH31749.1; -.
DR   EMBL; AK034731; BAC28810.1; -.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR003131; K_tetra.
DR   Pfam; PF02214; K_tetra; 1.
DR   SMART; SM00225; BTB; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   283 AA;  31886 MW;  7D67029CD51B8E2B CRC64;

  Query Match             9.1%;  Score 208.5;  DB 11;  Length 283;
  Best Local Similarity   26.0%;  Pred. No. 1.3e-10;
  Matches   74;  Conservative   42;  Mismatches  100;  Indels   69;  Gaps   10;

Qy         15 QGSAVPNSFPEV---VELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKG 71
              ||  :|    :    | ::||| :| :  :||   | | : ::|:       |  |
Db         43 QGIPLPAQLTKANAPVHIDVGGHMYTSSLATLTKYPDSRISRLFNGTEPIVLDSLKQ--- 99

Qy         72 RFFIDRDGFLFRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSP 131
               :|||||| :||||| :||  :::||| | :   |  || |:||  :|: |   :
Db        100 HYFIDRDGEIFRYILSFLRTSKLLLPDDFKDFNLLYEEARYYQLQPMVRELERWQ----- 154

Qy        132 DEFCHSDFEDASQGSDTRICPPSSLLPADRKWGFITVGYRGSCTLGREGQADAKFRRVPR 191
                     :|  |   :| |                :  | :  ||            |
Db        155 --------QDQEQRRRSRACD--------------CLVVRVTPDLGE-----------R 180

Qy        192 ILVCGRISLAKEVFGET---------LNESRDPDRAPERYTSRFYLKFKHLERAFDMLSE 242
              | : |  :| :||| ||            ::||     |:    | :   ::   : | :
Db        181 IALSGEKALIEEVFPETGDVMCNSVNAGWNQDPTHV-IRFPLNGYCRLNSVQ-VLERLFQ 238

Qy        243 CGFHMVA-CNSSVTASFINQYTDDKIWSSYTEYVFYREPSRWSPS 286
               || : | |   | :            | ::|||  ||  |  |:
Db        239 RGFSVAASCGGGVDS-----------SQFSEYVLCREERRPQPT 271


RESULT 13
Q8N3Q9
ID   Q8N3Q9      PRELIMINARY;      PRT;   216 AA.
AC   Q8N3Q9;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein (Fragment).
GN   DKFZP313I0334.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ansorge W., Wirkner U., Mewes H.W., Weil B., Wiemann S.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL832695; CAD38633.1; -.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR003131; K_tetra.
DR   Pfam; PF02214; K_tetra; 1.
DR   SMART; SM00225; BTB; 1.
KW   Hypothetical protein.
```

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FT   NON_TER       1      1
SQ   SEQUENCE   216 AA;  24790 MW;  1C6DC5158A3F1B2C CRC64;

  Query Match             8.9%;  Score 204;  DB 4;  Length 216;
  Best Local Similarity   42.7%;  Pred. No. 2.3e-10;
  Matches   47;  Conservative   20;  Mismatches   39;  Indels    4;  Gaps    1;

Qy         22 SFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFL 81
              |  |:| |||||::: || ||:   | | | :|     |  :   |   |: |:|||| |
Db          5 SSQELVTLNVGGKIFTTRFSTIKQFPASRLARML----DGRDQEFKMVGGQIFVDRDGDL 60

Qy         82 FRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSP 131
              | :|||:||  |::||  | :  ||:||| :::|  || || |  ::  |
Db         61 FSFILDFLRTHQLLLPTEFSDYLRLQREALFYELRSLVDLLNPYLLQPRP 110


RESULT 14
Q8IU75
ID   Q8IU75      PRELIMINARY;      PRT;   229 AA.
AC   Q8IU75;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Putative regulator of potassium channels protein variant 1 (Putative
DE   potassium channel proteins regulator protein variant A).
GN   KCNRG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Tyazhelova T.V., Ivanov D.V., Guskova A.A., Panchin Y.V.,
RA   Baranova A.V.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Tyazhelova T.V., Ivanov D.V., Baranova A.V.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY129653; AAN06090.1; -.
DR   EMBL; AY169387; AAO11777.1; -.
KW   Ionic channel.
SQ   SEQUENCE   229 AA;  25856 MW;  9065D19F89DEFA58 CRC64;

  Query Match             8.9%;  Score 204;  DB 4;  Length 229;
  Best Local Similarity   42.7%;  Pred. No. 2.4e-10;
  Matches   47;  Conservative   20;  Mismatches   39;  Indels    4;  Gaps    1;

Qy         22 SFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFL 81
              |  |:| |||||::: || ||:   | | | :|     |  :   |   |: |:|||| |
Db          2 SSQELVTLNVGGKIFTTRFSTIKQFPASRLARML----DGRDQEFKMVGGQIFVDRDGDL 57

Qy         82 FRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSP 131
              | :|||:||  |::||  | :  ||:||| :::|  || || |  ::  |
Db         58 FSFILDFLRTHQLLLPTEFSDYLRLQREALFYELRSLVDLLNPYLLQPRP 107
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RESULT 15
Q8N5I3
ID   Q8N5I3      PRELIMINARY;      PRT;   272 AA.
AC   Q8N5I3;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein BC013764 (Putative regulator of potassium
DE   channels protein variant 2) (Putative potassium channel proteins
DE   regulator protein variant B).
GN   KCNRG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Tyazhelova T.V., Ivanov D.V., Guskova A.A., Panchin Y.V.,
RA   Baranova A.V.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Tyazhelova T.V., Ivanov D.V., Baranova A.V.;
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC032343; AAH32343.1; -.
DR   EMBL; AY129654; AAN06091.1; -.
DR   EMBL; AY169388; AAO11778.1; -.
DR   InterPro; IPR000210; BTB_POZ.
DR   InterPro; IPR003131; K_tetra.
DR   Pfam; PF02214; K_tetra; 1.
DR   SMART; SM00225; BTB; 1.
KW   Hypothetical protein; Ionic channel.
SQ   SEQUENCE   272 AA;  31047 MW;  5018F55980F0BBA5 CRC64;

  Query Match             8.9%;  Score 204;  DB 4;  Length 272;
  Best Local Similarity   42.7%;  Pred. No. 3.1e-10;
  Matches   47;  Conservative   20;  Mismatches   39;  Indels    4;  Gaps    1;

Qy         22 SFPEVVELNVGGQVYFTRHSTLISIPHSLLWKMFSPKRDTANDLAKDSKGRFFIDRDGFL 81
              |  |:| |||||::: || ||:   | | | :|     |  :   |   |: |:|||| |
Db          2 SSQELVTLNVGGKIFTTRFSTIKQFPASRLARML----DGRDQEFKMVGGQIFVDRDGDL 57

Qy         82 FRYILDYLRDRQVVLPDHFPEKGRLKREAEYFQLPDLVKLLTPDEIKQSP 131
              | :|||:||  |::||  | :  ||:||| :::|  || || |  ::  |
Db         58 FSFILDFLRTHQLLLPTEFSDYLRLQREALFYELRSLVDLLNPYLLQPRP 107


Search completed: January 29, 2004, 02:55:16
Job time : 69 secs
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